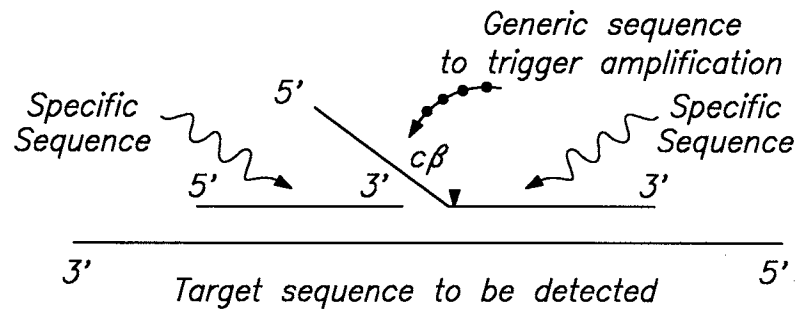
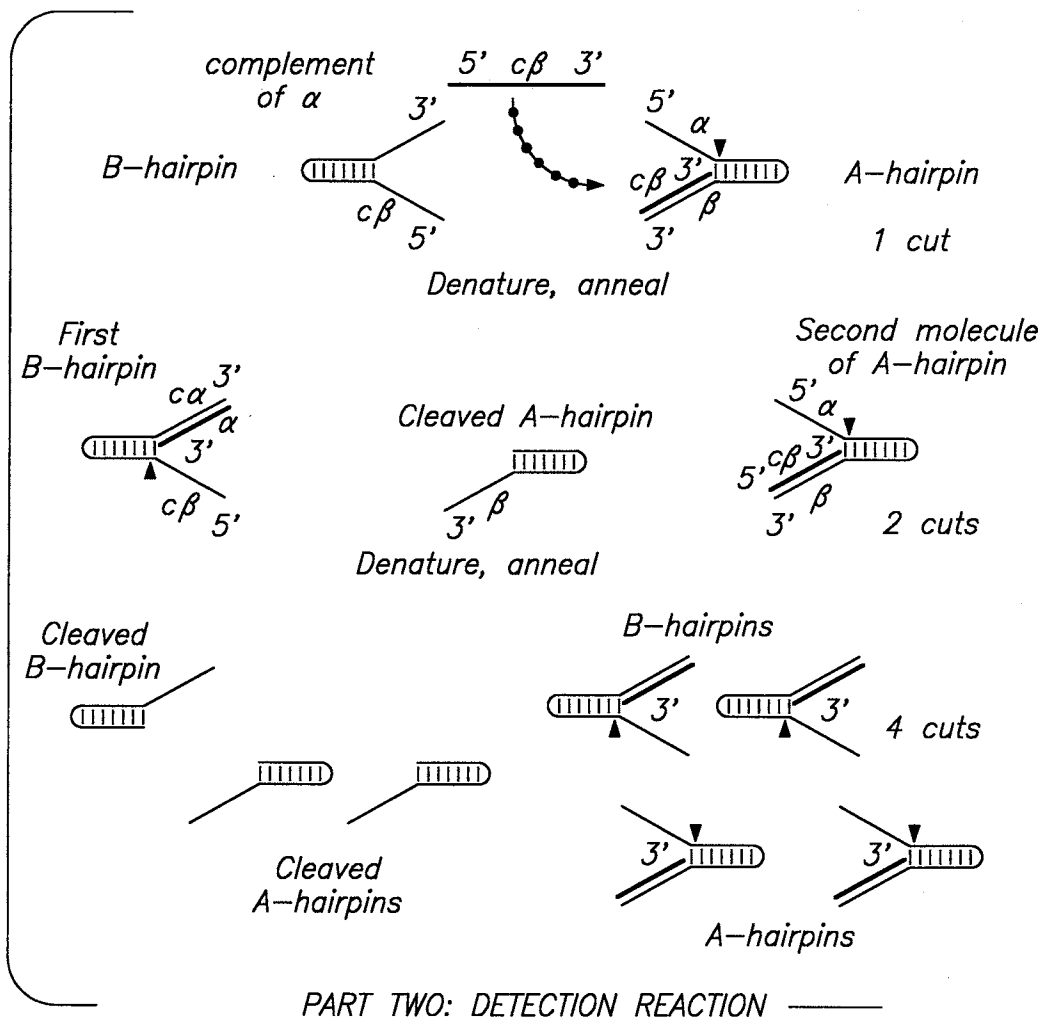


FIG. 1A

**FIG. 1B****PART ONE: TRIGGER REACTION****PART TWO: DETECTION REACTION**

## FIGURE 2

```

MAJORITY  CGAGGCGGACGACGTXCTGGCCACCCTGGCCAAGAGGCGGAAAGGAGGGGTACGAGGTGCGCATCCTC
DNAPTAQ   :.....C.....G.....C.....C..... 417
DNAPTFL   T.....G.....CG..... 414
DNAPTTH   :.....T..C..... 420

MAJORITY  ACCGCCGACCGGACCTCTACCAGCTCCTTTCCGACCGCATCGCCGTCCTCCACCCCGAGGGGTACCTCA
DNAPTAQ   :.....AA.....T.....CA..... 487
DNAPTFL   .T.....G.....G.....A.....T.....G. 484
DNAPTTH   :.....A..G.C.....G.....CC..... 490

MAJORITY  TCACCCCGCGGTGGCTTTGGGAGAGTAGTACGGCCTGAGGCCGGAGCAGTGGGTGGACTACCGGGCCCTGGC
DNAPTAQ   :.....C.....A.....C..C.....CC.....A. 557
DNAPTFL   :.....AC.....C.C.....T..C.....C.T 554
DNAPTTH   :.....A.....C..... 560

MAJORITY  GGGGGACCCCTCCGACAACCTCCCCGGGGTCAAGGGCATCGGGGAGAGACCGCCXGAAGCTCCTCXAG
DNAPTAQ   C.....GAG.....T.....G..GAG.....T..GG.. 627
DNAPTFL   :.....G..T..A.....G.....A..G...A..CGC 624
DNAPTTH   :.....:.....TC.....A.. 630

MAJORITY  GAGTGGGGAGCCTGGAAACCTCCTCAAGAACCTGGACCGGTGAAGCCCGC...CXTCCGGGAGAAGA
DNAPTAQ   :.....GC.....C.....A..... 694
DNAPTFL   :.....T..C..C.....A.....T.....T.G.....C 691
DNAPTTH   :.....A.....:.....A..A.AAA.G..... 700

```

FIGURE 2 (cont.)

```

MAJORITY  TCCAGGCCACATGGAXGACCTGAXGCTCTCCTGGGAGCTXTCCCAGGTGCGCACCCGACCTGCCCTGGA
DNAPTAQ   ...T...C..T...A...C..GG..A...C...T...764
DNAPTFL   ...GGG...G.C...GCC..T...C..A...T...A..T...761
DNAPTTH   ..A...C...A...C.G...T...C...G...C...C...770

MAJORITY  GGTGGACTTCGCCAAGXGGCGGGAGCCCGACCGGGAGGGGCTTAGGGCCTTTCTGGAGAGGCTGGAGTTT

DNAPTAQ   ...AA...AA...A...A...T...T...T...834
DNAPTFL   ...GG.G.C.C..CACA..A...T...T...T..GC...T...C..T...831
DNAPTTH   ...C...C.G...C...C...C...C...C...C...C...840

MAJORITY  GGCAGCCTCCTCCACGAGTTCGGGCTCCTCGGAGGGCCCCCAAGGCCCTGGAGGAGGCCCTGCCCCCGC

DNAPTAQ   ...T...T...AA...T...T...T...T...904
DNAPTFL   ..A...G...G...G...G...G...G...G...G...T...901
DNAPTTH   ...C...C...C...C...C...C...C...C...C...910

MAJORITY  CGGAAGGGGCTTCGTGGGCTTTGTCTCTTTCCCGCCCCGAGCCCATGTGGGCCGAGCTTCTGGCCCTGGC

DNAPTAQ   ...T...T...G...G...AAG...T...T...974
DNAPTFL   ...T..TT...TC.T...T...T...T...T...971
DNAPTTH   ...C...C...C...C...G...G...G...G...AAA...980

MAJORITY  CGCCGCCAGGGGCGGGTCCACCGGGCACCAAGACCCCTTTAXGGGCTTAXGGGACCTXAAGGAGGTG

DNAPTAQ   ...G...G...C..C..G..T.A..AA.C...C...G...C...1044
DNAPTFL   T.GG..GT...G..CC...T...A...C...G...G...T...G...1041
DNAPTTH   ...TG...C...G...G...G...G...G...G...G...C...C...1050

```

FIGURE 2 (cont.)

```

MAJORITY  CGGGGXCTCCTCGCCAAGGACCTGGCCGTTTTGGCCCTGAGGGAGGGCCTXGACCTCXTGCCCCGGGGACG

DNAPTAQ   .....G..T.....A.....AG....C.....A.....T.G....CC.....C.... 1114
DNAPTFL   ....AA....G.....G.....C.....G.....T.C..A.A.... 1111
DNAPTTH   .....C.....C.....TC.....G.A.....G..... 1120

MAJORITY  ACCCCATGCTCCTCGCCTACCTCCTGGACCCCTCCAACACCACCCCGAGGGGTGGCCCCGGCGCTACGG

DNAPTAQ   .....T.....T.....T.....T.....T.....T..... 1184
DNAPTFL   .....G.....T.....T.....T.....T.....T..... 1181
DNAPTTH   .....T.....T.....T.....T.....T.....T..... 1190

MAJORITY  GGGGGAGTGGACGGAGGAXGCGGGGGAGCGGGCCCTCCTXTCCGAGAGGCTCTTCCXGAACCTXXXGGAG

DNAPTAQ   C.....G.....G.....GC...T.....GC...T.....GCC....GTG..G. 1254
DNAPTFL   .....T.....A.....GG....C.C....C.C....A..C...AAA.... 1260
DNAPTTH   .....C..C.CCC.C.....C..G.....CAT.G.....CCTTA.. 1260

MAJORITY  CGCCTTGAGGGGGAGGAGGCTCCTTTGGCTTTACCGAGAGGTGGAGAAGCCCCCTTTCCCGGGTCCIGG

DNAPTAQ   A.G.....A.....G.....G.....G.....GCT..... 1324
DNAPTFL   .....A...A..A..AC.C..G.....G.....G.....GT... 1321
DNAPTTH   .....C.....A.....C.....C.....A.....C..... 1330

MAJORITY  CCCACATGGAGGCCACGGGGGTXCGGGCTGGACGTGGCCTACCTCCAGGCCCTXTCCCTGGAGGTGGCGGA

DNAPTAQ   .....G.....G..C.....T...AG....T.G.....C.. 1394
DNAPTFL   ...GG.....C.....C.....C.....A..C 1391
DNAPTTH   .....C.....A.....T.....T.....C.T..... 1400

```

FIGURE 2 (cont.)

MAJORITY	GGAGATCCGGCCGCTCGAGGAGGAGGTCTTCCGCTGGCCGGCCACCCCTTCAACCTCAACTCCCGGGAC	
DNAPTAQ	.....GC.....CC.....	1464
DNAPTFL	.....G.G....AG..G.....C....	1461
DNAPTTH	.....T.....G.....	1470
MAJORITY	CAGCTGGAAAGGTGCTCTTTGACGAGCTXGGGCTTCCCGCCATCGGCAAGACGGAGAAGACXGGCAAGC	
DNAPTAQ	.....C.....A.....C.....	1534
DNAPTFL	.....GC.....G.C..G..T.....G..G..A..	1531
DNAPTTH	.....TA.....T.G..G.....C.A.....A.....	1540
MAJORITY	GCTCCACGAGCGCCGCTGCTGGAGGCCCTXCGXGAGGGCCCAACCCCATCTCGTGGAGAAGATCCTGCAGTA	
DNAPTAQ	.....C.....C..C.....	1604
DNAPTFL	.....T.....G..A.....CCGC.....	1601
DNAPTTH	.....G.....A..G.....C...C..	1610
MAJORITY	CCGGGAGCTCACCAAGCTCAAGAACACCTACATXGACCCCTGCCCXGXCCCTCGTCCACCCAGGACGGGC	
DNAPTAQ	.....G...G.....T.....G.A...A.....	1674
DNAPTFL	.....A.....C.C...G.....A...C...C....	1671
DNAPTTH	.....G.G.....AAG.....G.....	1680
MAJORITY	CGCCTCCACACCCGCTTCAACCAGACGGCCACGGCCACGGGCAGGCTTAGTAGCTCCGACCCCAACCTGC	
DNAPTAQ	.....A.....A.....T.....C..	1744
DNAPTFL	.....G.....C.....TCC.....	1741
DNAPTTH	.....G.....G.....	1750

FIGURE 2 (cont.)

```

MAJORITY AGAACATCCCCGTCCGCACCCXCTGGGCCAGAGGATCCGCCGGGCCCTTCGTGGCCCGAGGAGGGXTGGGT

DNAPTAQ .....G..T..G.....A.C.....G...C. 1814
DNAPTFL .....G.....T.....C.C.....A.....C..... 1811
DNAPTTH .....CT.....C.....T.....C..... 1820

MAJORITY GTTGGTGGCCCTGGACTATAGCCAGATAGAGCTCCGGGTCTCTGGCCCCACCTCTCCGGGGACGAGAACCTG

DNAPTAQ A.....T.T.....C.....A.....G.....C..... 1884
DNAPTFL .C.....T.T.....C.....T.....C..... 1881
DNAPTTH .....A.....A.....C.....C.....A..... 1890

MAJORITY ATCCGGGTCTTCCAGGAGGGGAGGACATCCACACCCAGACCGCCAGCTGGATGTTCCGGCGTCCCCCCCCG

DNAPTAQ .....T.....C.....C.....GG.....G... 1954
DNAPTFL .....T.....T.....TT.....C. 1951
DNAPTTH .....A.....A.....A..... 1960

MAJORITY AGGCCGTGGACCCCTGATGCGCCGGCGGCCAAGACCATCAACTTCGGGGTCCTCTACGGCATGTCCGC

DNAPTAQ .....A.GG..A.....T.....G... 2024
DNAPTFL .....A.GG..A.....T.....G.....G..... 2021
DNAPTTH .....TA.G.....GG.....GG.G.....C..... 2030

MAJORITY CCACCGCCTCTCCCAGGAGCTTGCCCATCCCCCTACGAGGAGGCGGTGGCCTTCATTGAGCGCTACTTCCAG

DNAPTAQ .....A.....A.....T.....CCA.....T... 2094
DNAPTFL .....GG.....T.....T..... 2091
DNAPTTH .....TA.G.....T.A.....A 2100

```

FIGURE 2 (cont.)



```

MAJORITY AGCTTCCCCAAGGTGCGGGCCTGGATTGAGAAAGACCCTGGAGGAGGGCAGGAGCGGGGGTACGTGGAGA
DNAPTAQ ..... 2164
DNAPTFL ...A.....GG.....C.....C.CC.....T..... 2161
DNAPTTH .....A.A.....G.....A.....C.....A. 2170

MAJORITY CCCTCTTCGGCCGCGGCTACGTGCCCCGACCTCAACGCCCGGGTGAAGAGCGTGCGGGAGGCGGCGGA
DNAPTAQ .....C.....A.....AG.G.....C..... 2234
DNAPTFL .....T.....C.....C..... 2231
DNAPTTH .....AA.AA.....CA.....C..... 2240

MAJORITY GCGCATGGCCTTCAACATGCCCGTCCAGGGCACCCGCCGACCTCATGAAGCTGGCCATGGTGAAGCTC
DNAPTAQ .....T..... 2304
DNAPTFL .....G.....CG...T 2301
DNAPTTH .....C..... 2310

MAJORITY TTCCCCCGGCTXCAGGAAATGGGGGCCAGGATGCTCCTXCAGGTCCACGACGAGCTGGTCTCGAGGCC
DNAPTAQ .....A...GG.....T..... 2374
DNAPTFL .....T.....C.....G.....TT.G.....G..... 2371
DNAPTTH .....C.C.G...G.....C.C.....C.....G..... 2380

MAJORITY CCAAAGAGCGGCGGAGGXGGTGGCCGCTTTGGCCAAAGGAGGTTCATGGAGGGGTCTATCCCCCTGGCCGT
DNAPTAQ .....A.....A.....CC.....CGGC.....G..... 2444
DNAPTFL .....G..C.....AG..A.....C.....GG.....CAG.. 2441
DNAPTTH ..C...C.....C...A.....G.....C.....AA..C.....C..... 2450

```

FIGURE 2 (cont.)

MAJORITY	GCCCCTGGAGGTGGAGGTGGGGATGGGGGAGGACTGGCTCTCCGCCCAAGGAGTAG	
DNAPTAQ	.....A.....GA	2499
DNAPTFL	.....CC.....	2496
DNAPTTH	.....T.....GT...	2505

FIGURE 2 (cont.)

MAJORITY MXAMLPLFEPKGRVLLVDGHHLAYRTFFALKGLTTSRGEPVQAVYGFAKSLLKALKEDG·DAVXVVVFDK

TAQ PRO .RG.....H.....I..... 69  
 TFL PRO .....V.V..... 68  
 TTH PRO .E.....YK..F..... 70

MAJORITY APSFRHEAYEAYKAGRAPTPEDFPROLALIKELVDLLGLXRLEVPGYEADDVLATLAKKAEKEGYEVRIL

TAQ PRO .....GG.....A.....S..... 139  
 TFL PRO .....V.....F.....R..... 138  
 TTH PRO .....FT..... 140

MAJORITY TADRDLYQLLSDRIAVLHPEGYLITPAWLWEKYGLRPEQWVDYRALXGDPDSNLPGVKGIGECTAXKLLX

TAQ PRO .....K.....H.....D..A.....T..E.....R...E 209  
 TFL PRO .....E...I.....Y.....A.....I.....QR..IR 208  
 TTH PRO .....V...V.....H...E...F...V.....L...K 210

MAJORITY EWGSLLENLLKNLDRVKP·XXREKIXAHMEDLXLSSXLSXVRTDLPLEVDFAXRREPDRGLRAFLERLEF

TAQ PRO .....A.....L...AI.....L...D...K..WD.AK.....K.....R..... 278  
 TFL PRO .....FQH...Q...SL...LQ.G..A.A..RK..Q.H.....GR..T.NL..... 277  
 TTH PRO .....ENV.....K..L...R..LE..R.....L.QG..... 280

MAJORITY GSLLHEFGLLEXPKALEEAPWPPPEGAFVGFVLSRPEPMWAEALLALAAARXGRVHRAXDPLXGLRDLKEV

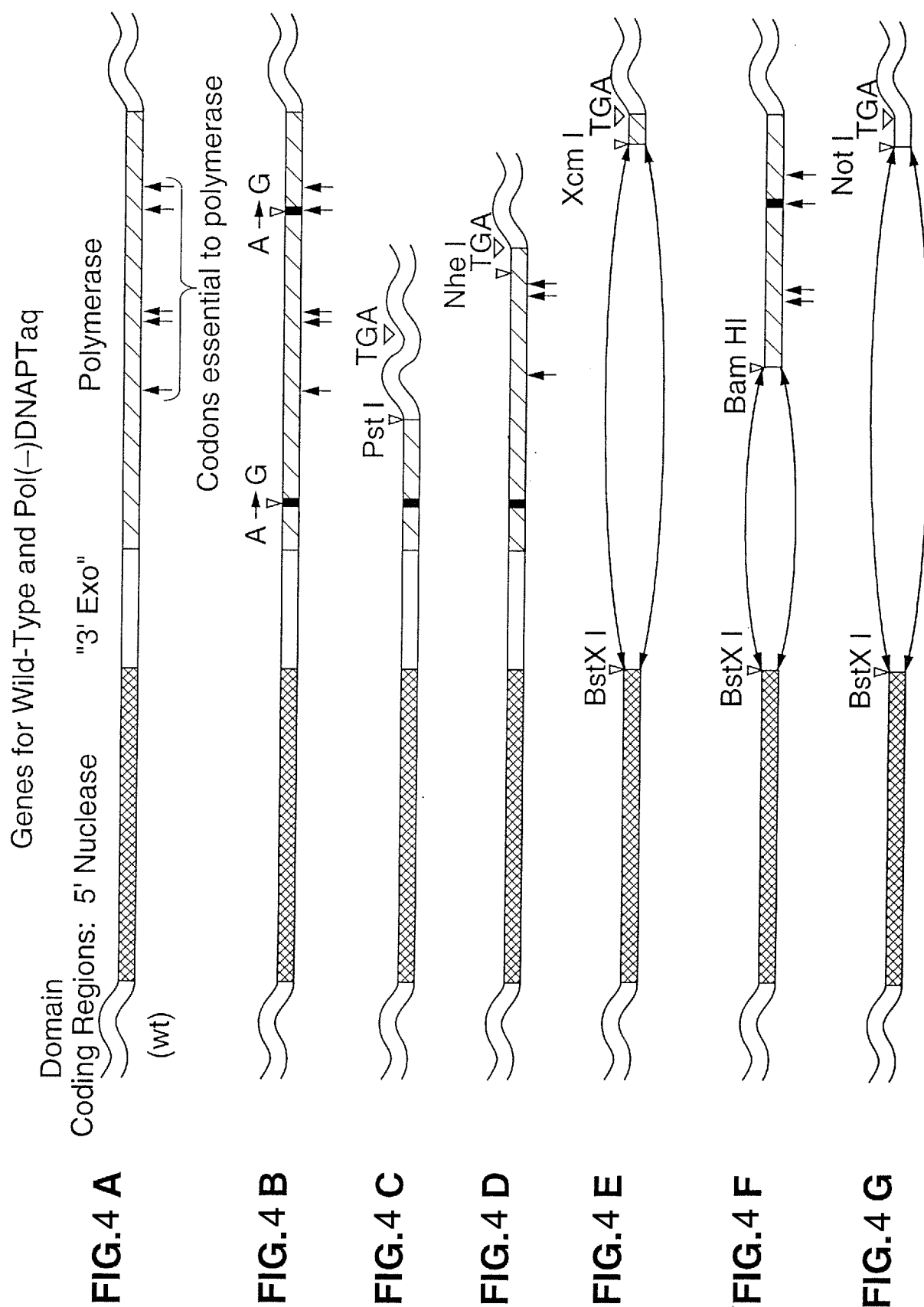
TAQ PRO .....S.....K.....D.....PE.YKA.....A 348  
 TFL PRO .....G..A.....L..SF.....G.WE..L...Q...R.....G.. 347  
 TTH PRO .....A.AP.....K.....C.D.....A...A..K..... 350

FIGURE 3

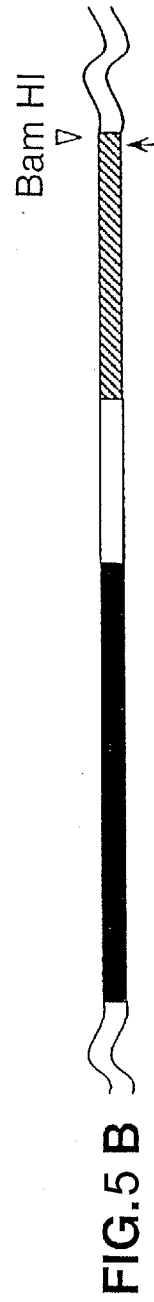
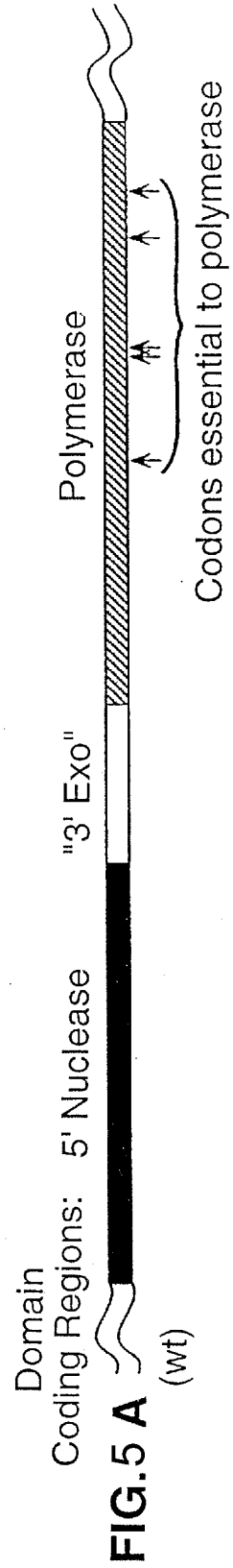
MAJORITY		RGLLAKDLAVLALREGLDLXPGDDPMLLAYLLDPSNTTPEGVARRYGGEWTEAGEDALLSERLFXNLXX	
TAQ	PRO	.....S.....G.P.....E.....A.....A.....WG	418
TFL	PRO	..I.....F.E.....A.....QT.KE	417
TTH	PRO	.....S.....V.....AH.....HR..LK	420
MAJORITY		RLEGEERLLWLYXEVEKPLSRVLAHMEATGVRLDVAYLQALSLEVAEEIRLEEVEFRLAGHPFNLNSRD	
TAQ	PRO	.....R.....R.....A.....R.....A.....A.....	488
TFL	PRO	..K.....E.....R.....EA.V.Q.....	487
TTH	PRO	.....K.....H.....L.....	490
MAJORITY		QLERVLFDELGLPAIGKTEKTKRSTSAAVLEALREAHPIVEKILQYRELTKLKNITYIDPLPXLVHPRTG	
TAQ	PRO	.....R.....L.....Q.....S.....D.I.....	558
TFL	PRO	.....R.....L.....Q.....DR.....A.....K.....	557
TTH	PRO	.....R.....L.....Q.....H.....V.....S.....	560
MAJORITY		RLHTRFNQTATATGRLSSSDPNLQNIPTPLGQIRRAFVAEEGWXLVALDYSQIELRVLAHLSGDENL	
TAQ	PRO	.....I.....L.....	628
TFL	PRO	.....V.....V.....	627
TTH	PRO	.....A.....A.....	630
MAJORITY		IRVFQEGRDIHTQTASWMFGVPPEAVDPLMRRAAKTINFGVLYGMSAHRLSQELAIPYEEAVAFIERYFQ	
TAQ	PRO	.....E.....R.....Q.....	698
TFL	PRO	.....S.....G.....G.....S.....	697
TTH	PRO	.....K.....V.....	700

FIGURE 3 (cont.)

FIGURE 3 (cont.)



## Genes for Wild-Type and Pol(-)DNAPTfl



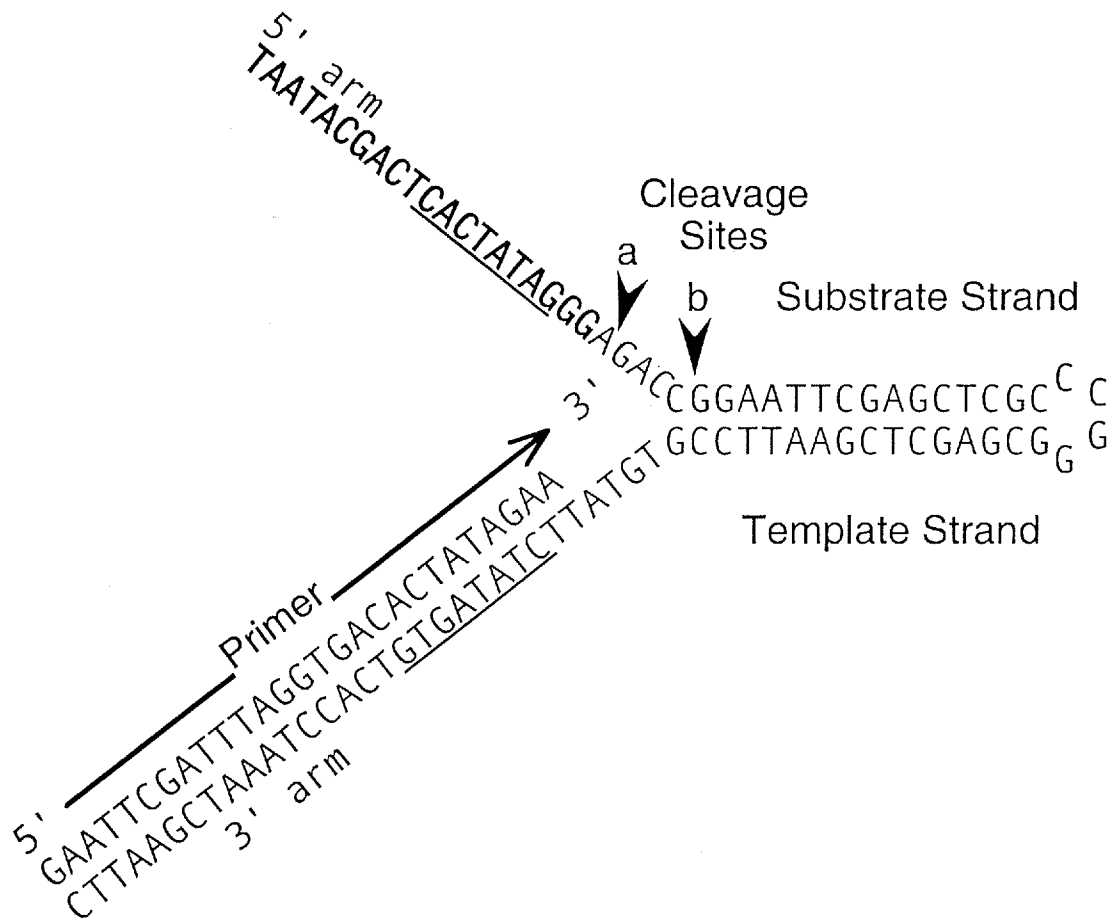


FIGURE 6



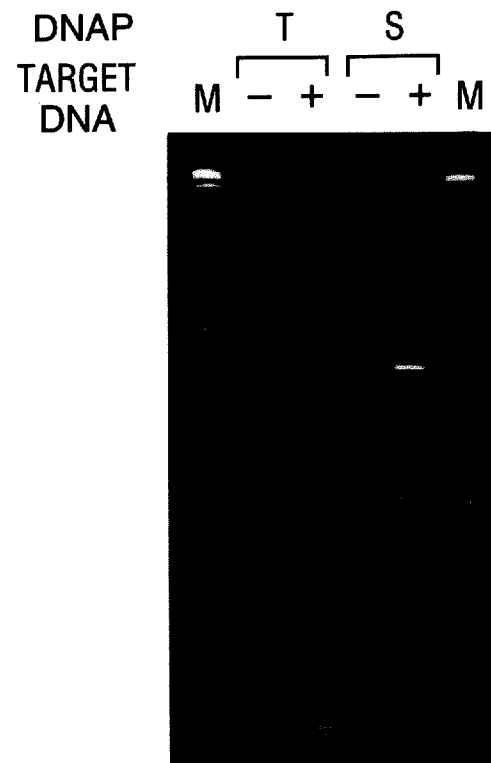


FIGURE 7

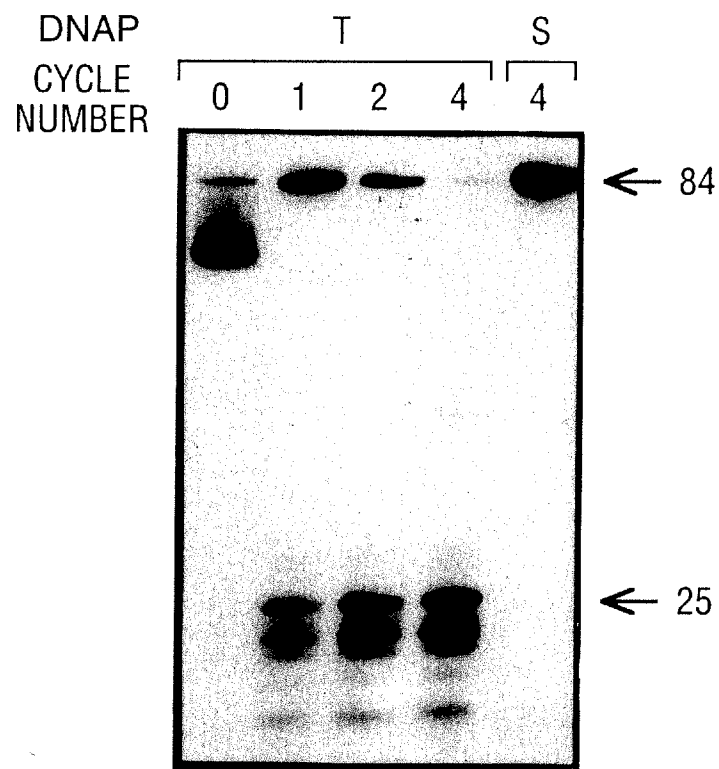


FIGURE 8

	1	2	3	4	5	6
DNAP-T:	-	+	+	+	+	+
MgCl <sub>2</sub> :	+	-	+	+	+	+
dNTPs:	+	-	+	-	+	-
Primers:	+	-	+	+	-	-

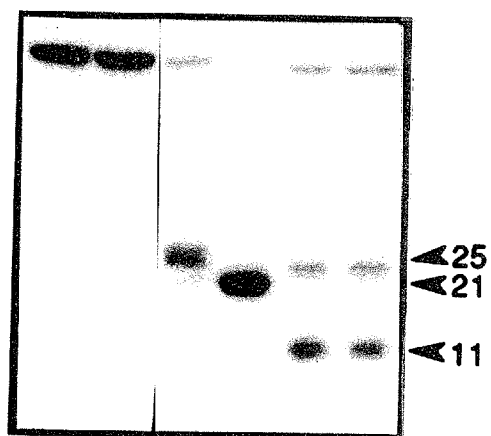


FIG. 9A

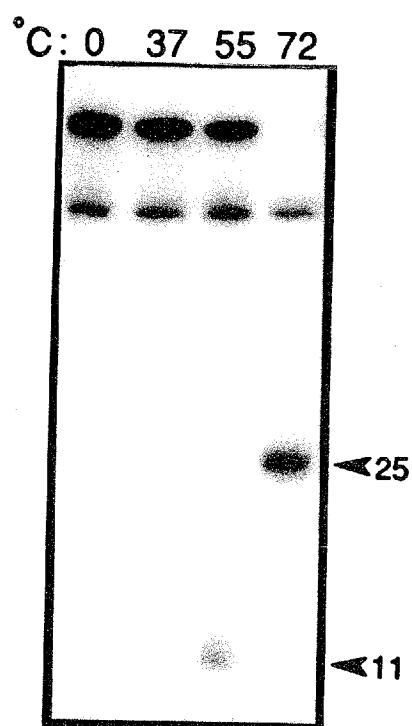


FIG. 9B

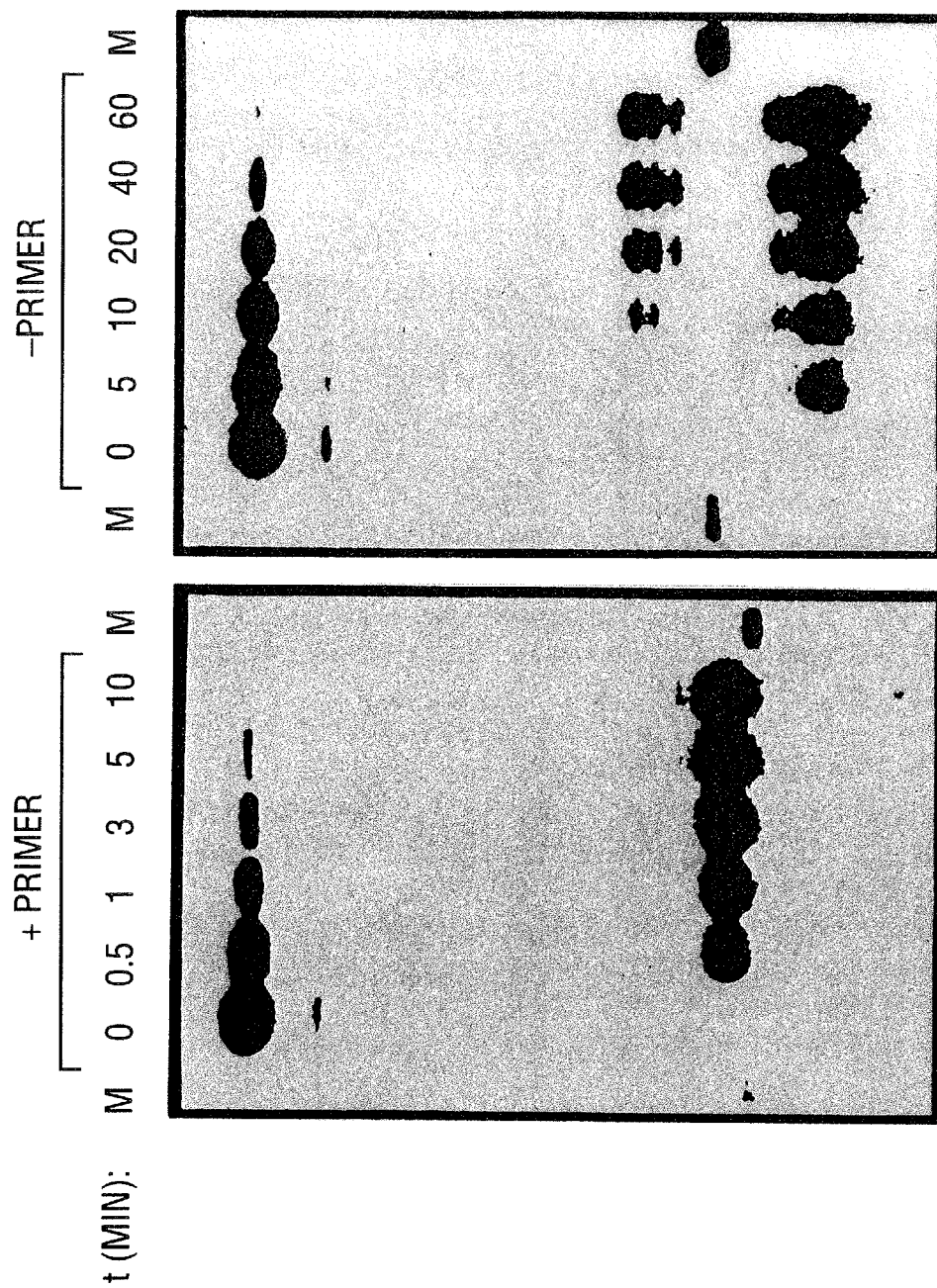


FIG. 10A

FIG. 10B

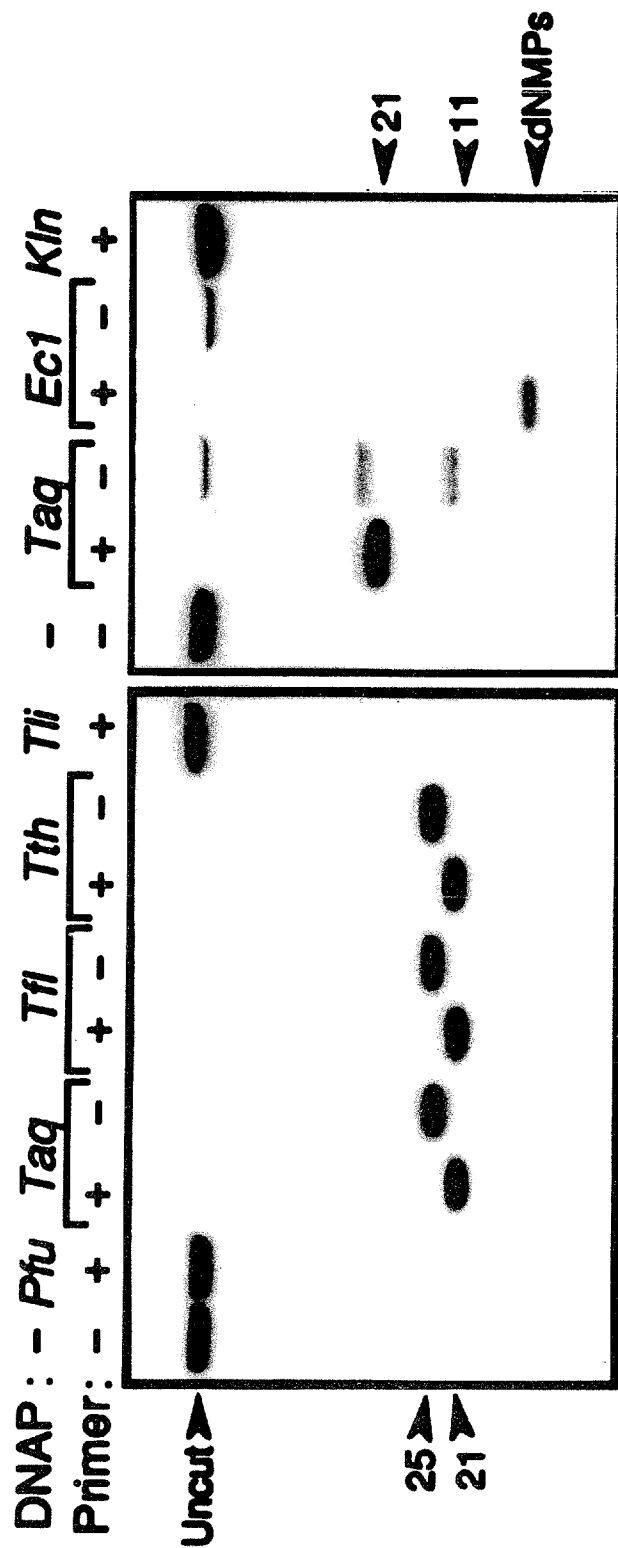


FIG. 11A

FIG. 11B

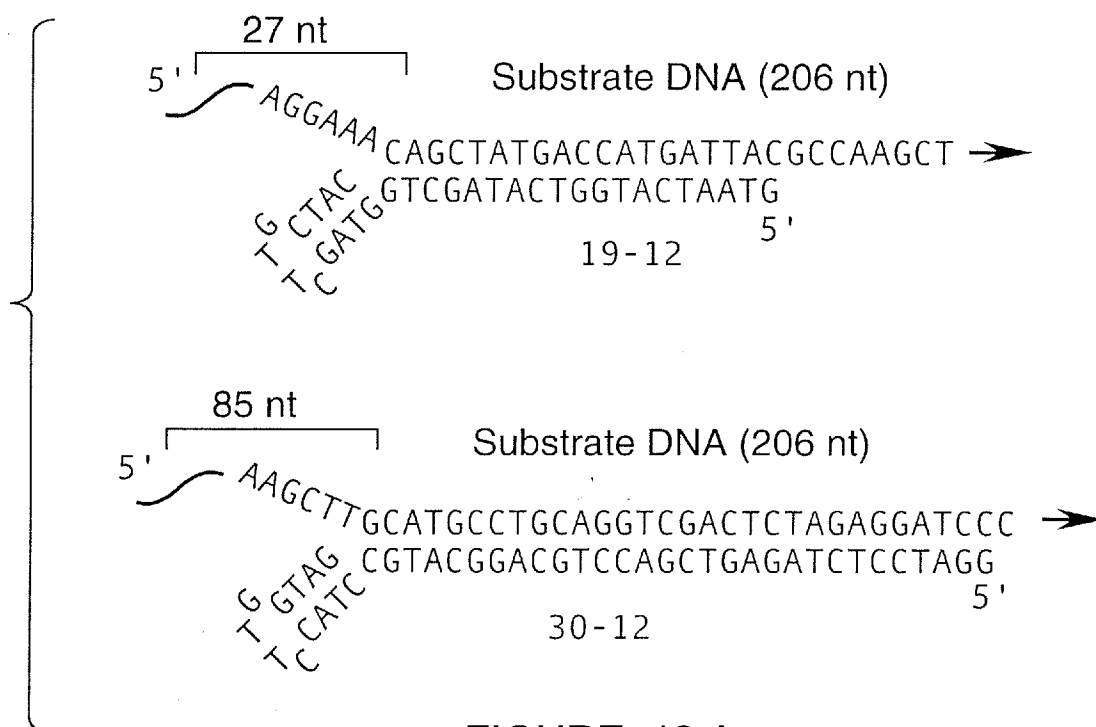


FIGURE 12 A

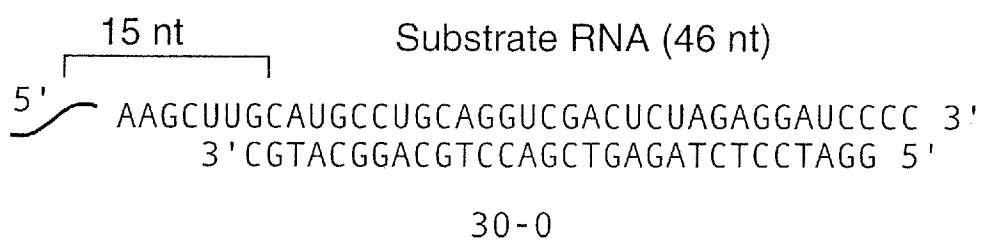


FIGURE 13 A

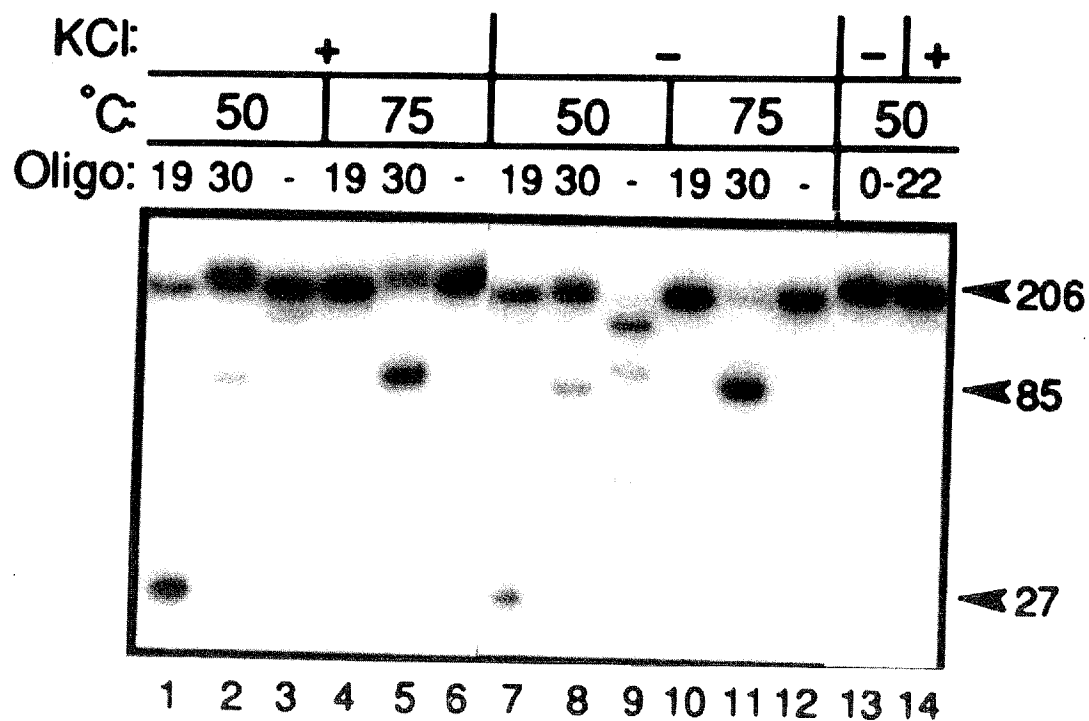
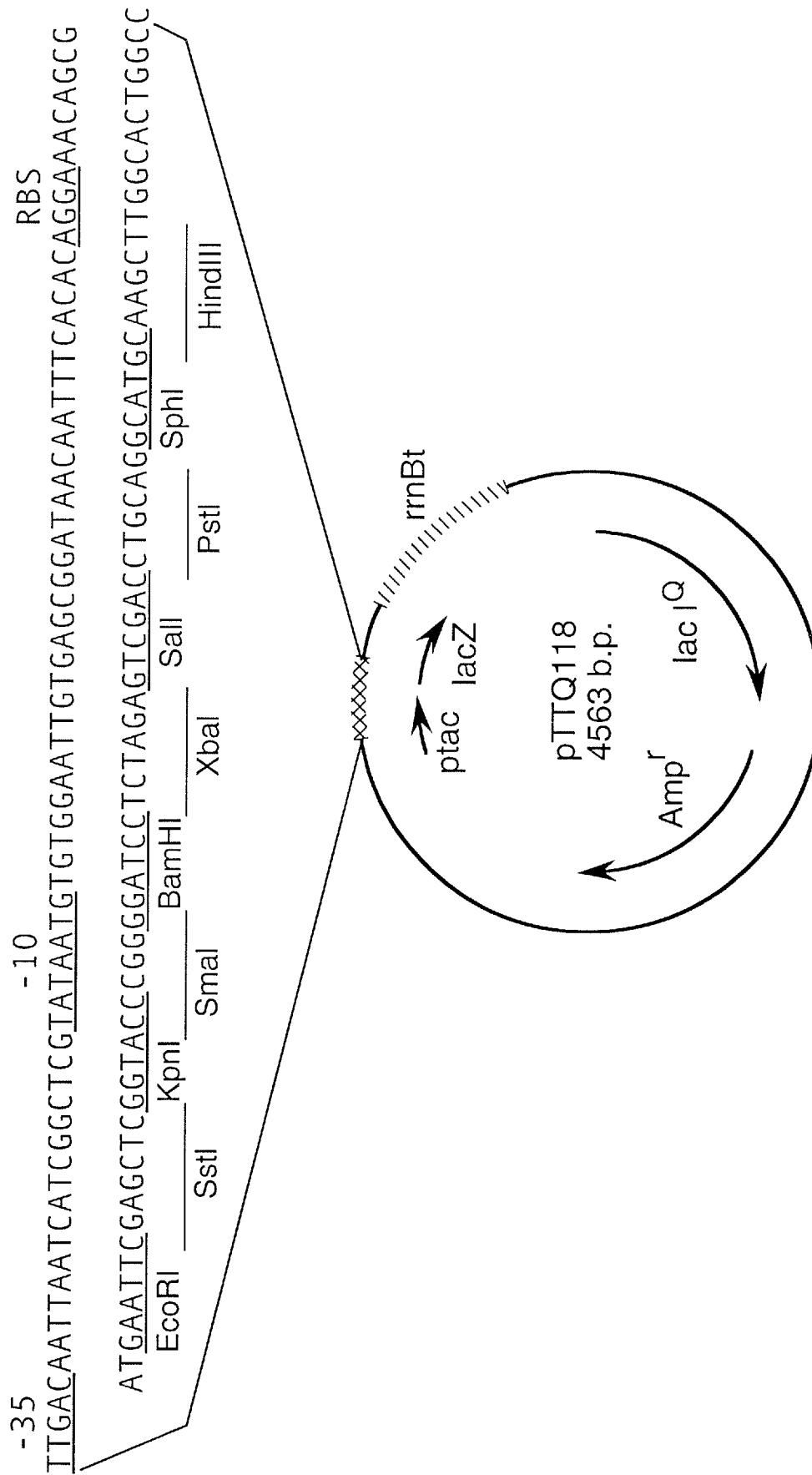


FIG. 12B



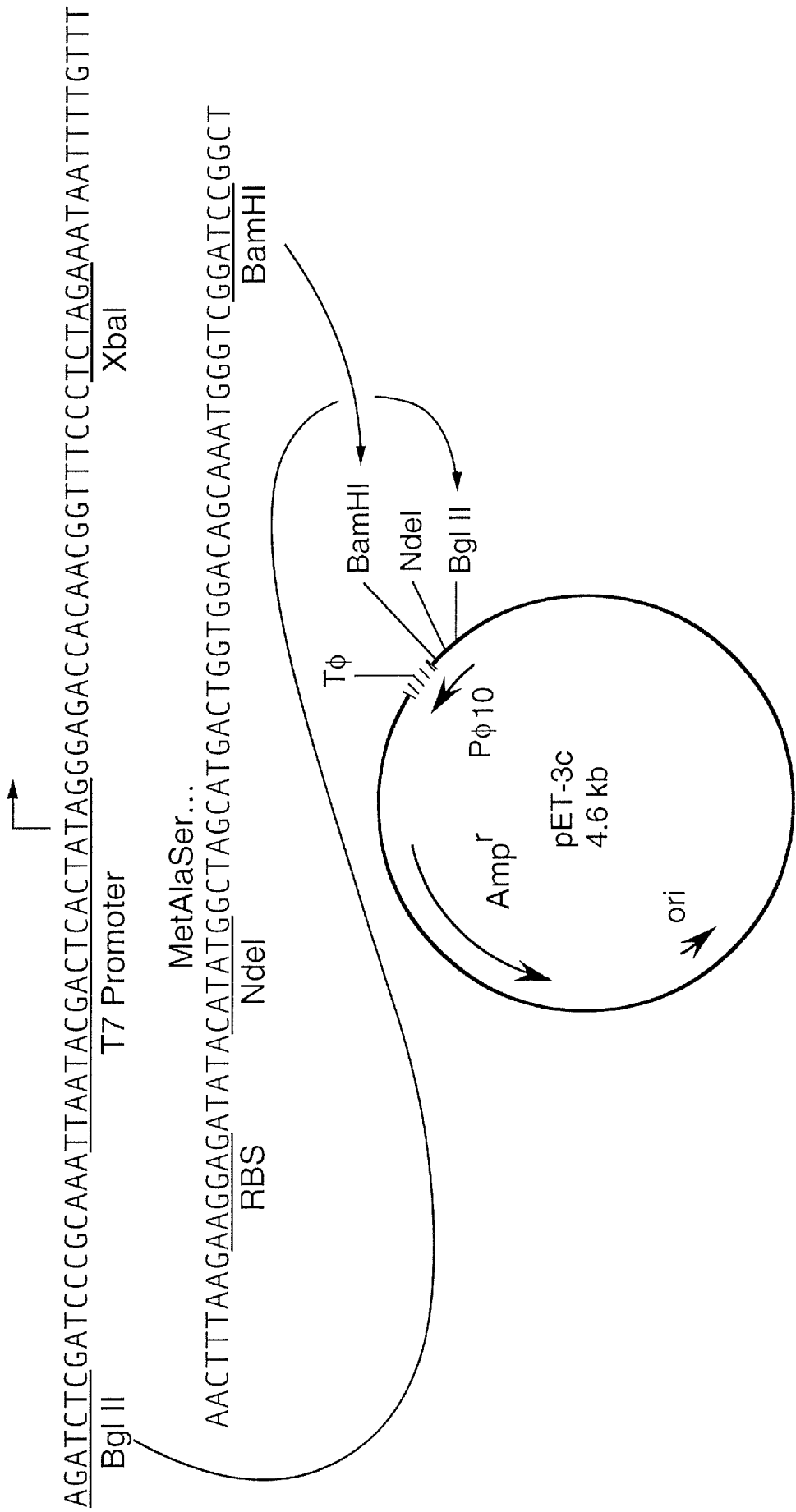
FIG. 13B



RBS: Ribosome binding site      lacZ: Beta-galactosidase alpha fragment  
 ptac: Synthetic tac promoter      rrnBt: E. coli rrnB transcription terminator  
 lac I<sup>Q</sup>: Lac repressor gene

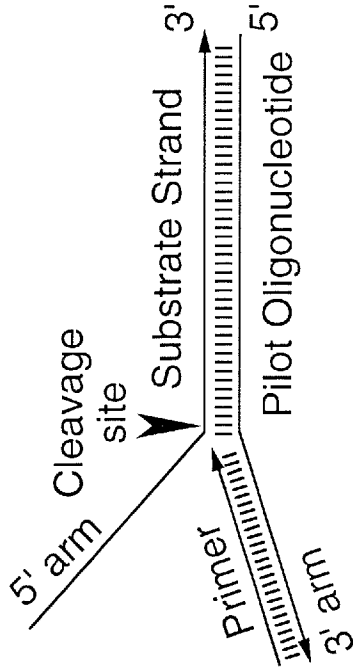
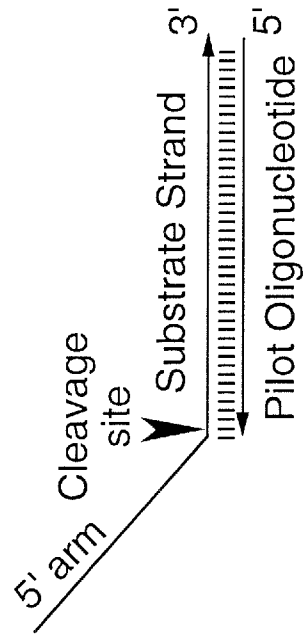
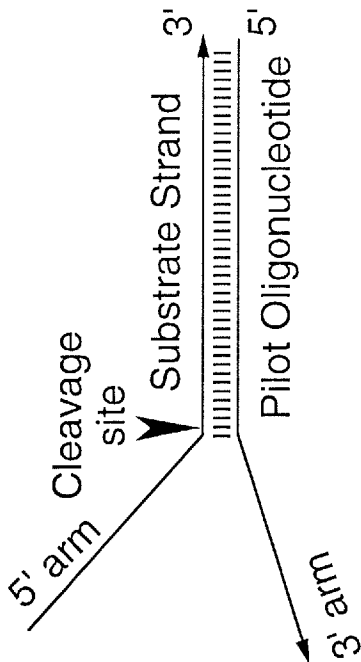
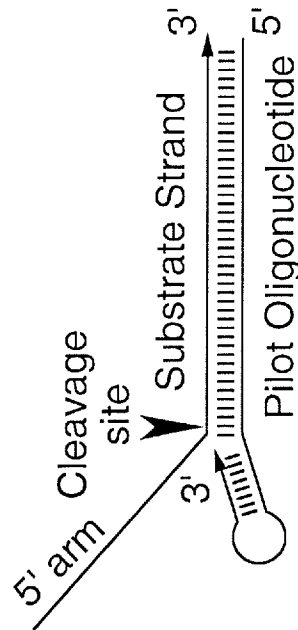
FIGURE 14





P<sub>φ10</sub>: Bacteriophage T7  $\phi$ 10 promoter      RBS: Ribosome binding site  
 T<sub>φ</sub>: T7  $\phi$  Terminator

FIGURE 15

**FIG. 16B****FIG. 16D****FIG. 16A****FIG. 16C**

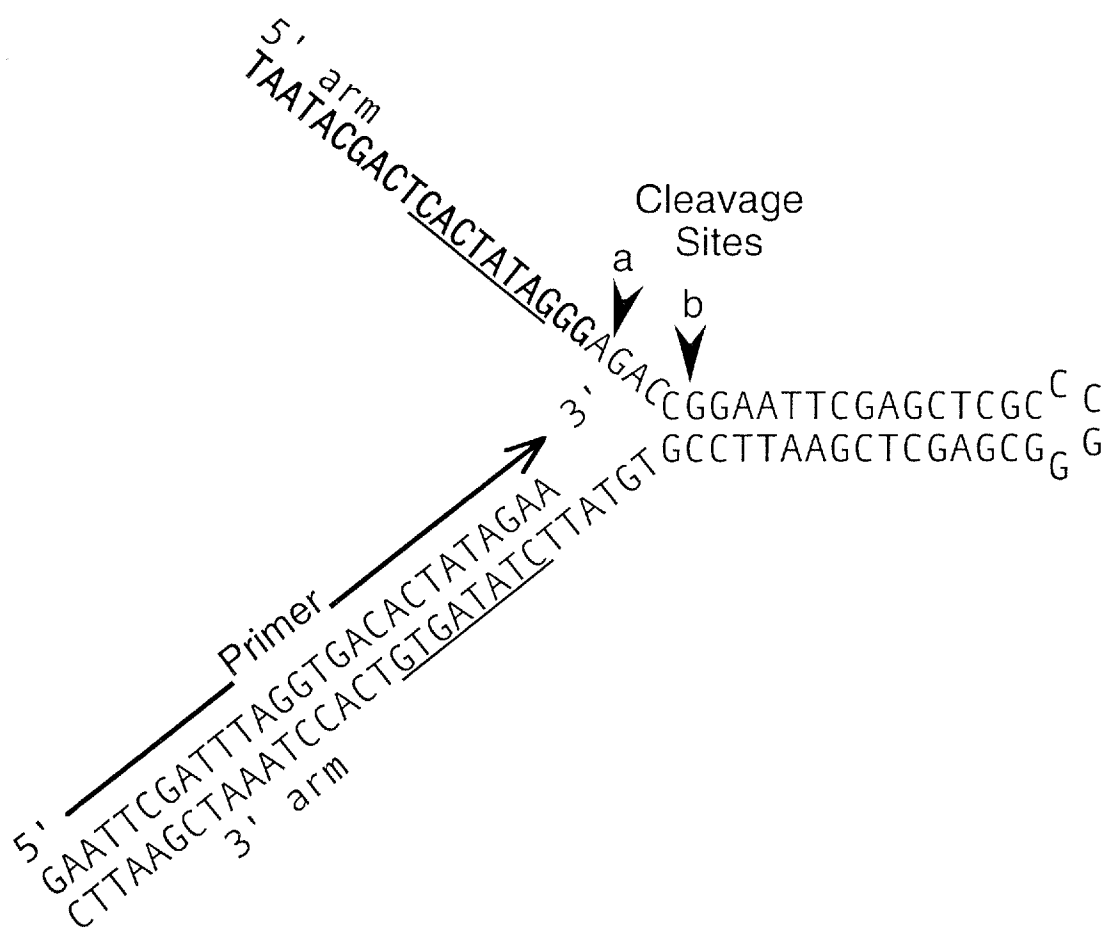


FIGURE 16 E

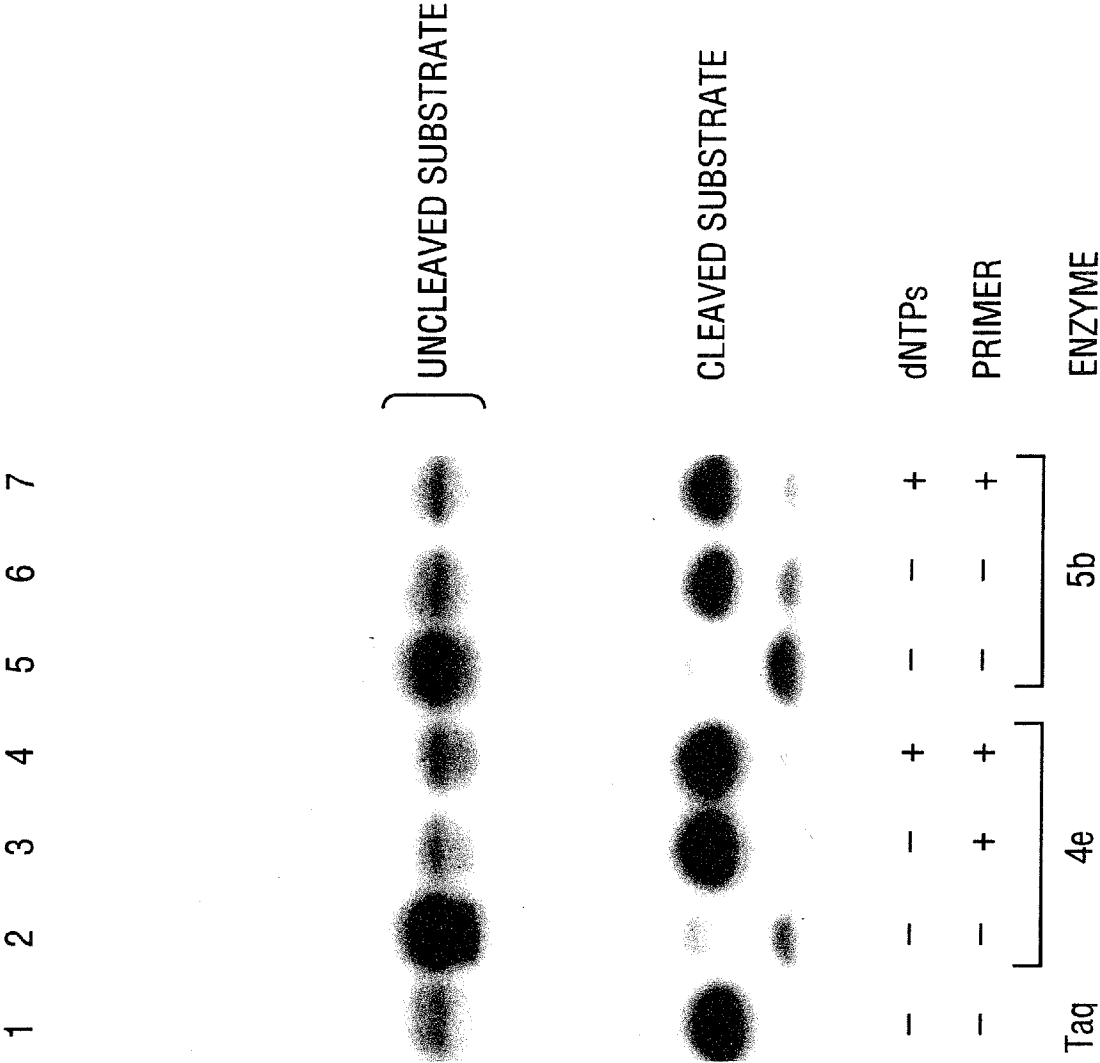
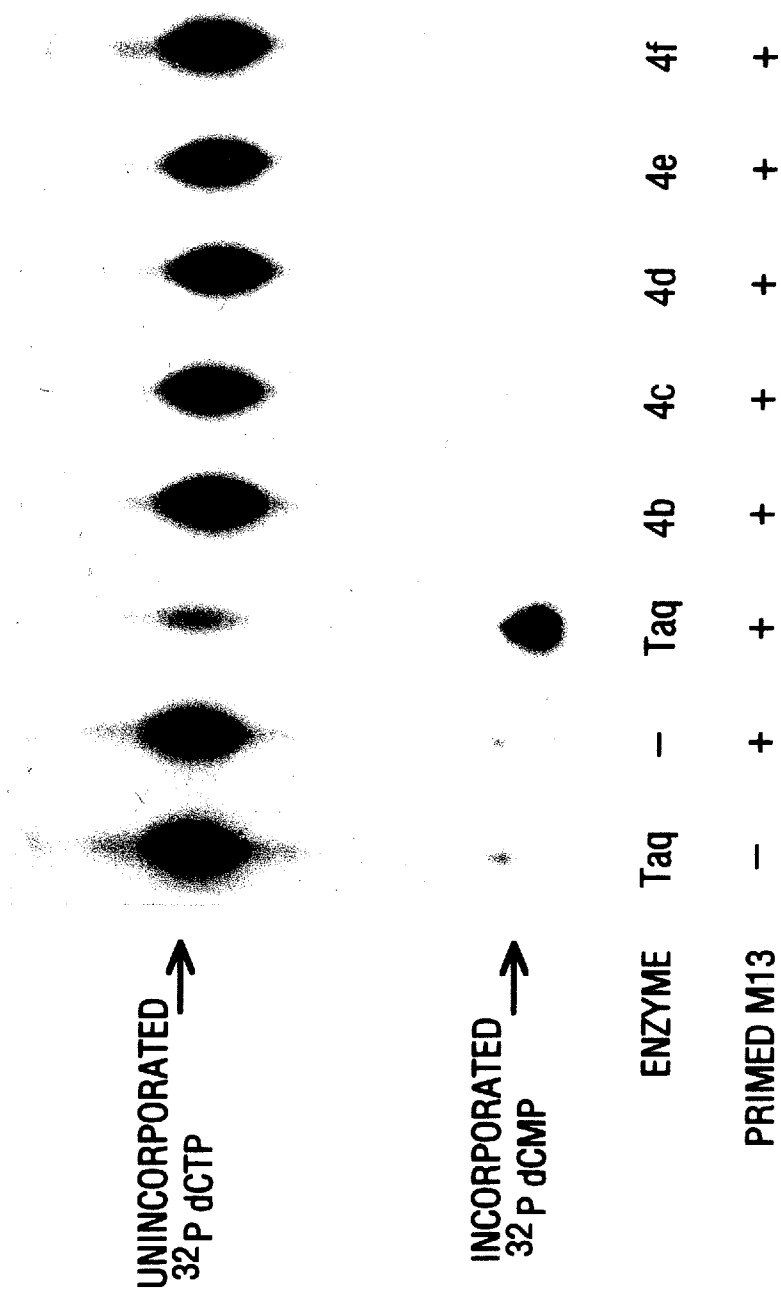


FIG. 17



**FIG. 18**

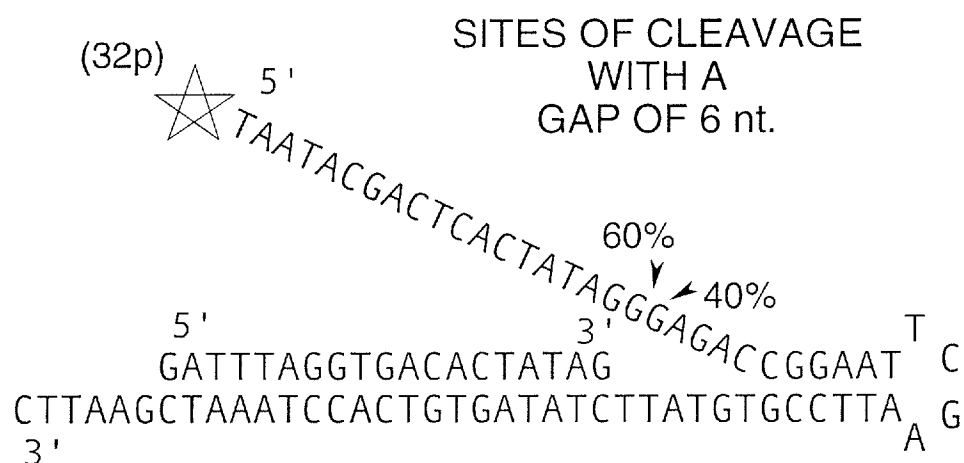


FIGURE 19 A

**SOME ABERRANT CLEAVAGE WITH "4b"  
BECAUSE OF RESIDUAL POLYMERASE ACTIVITY.**

**FIG. 19B**

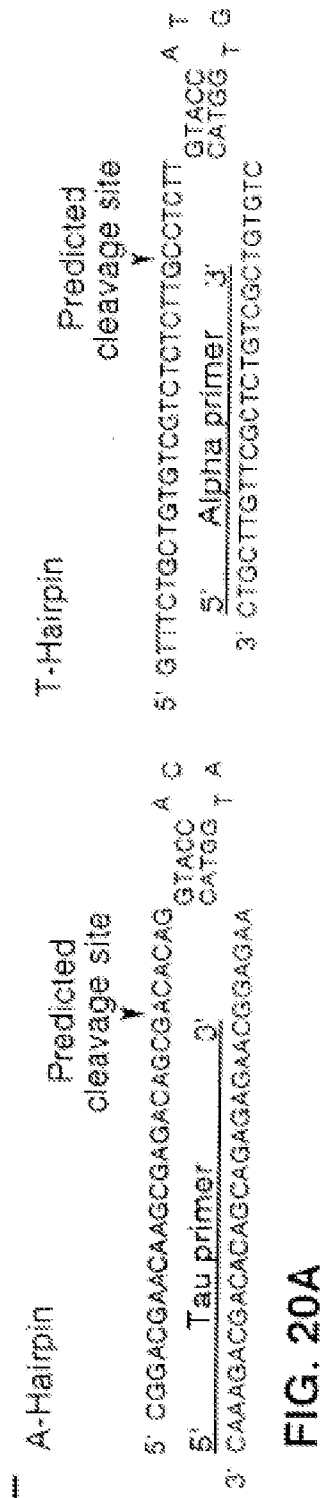


FIG. 20A

Sequence of alpha primer:



2023

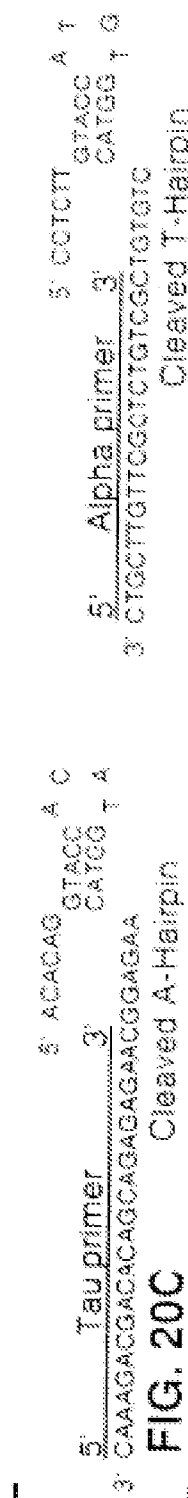


FIG. 20C

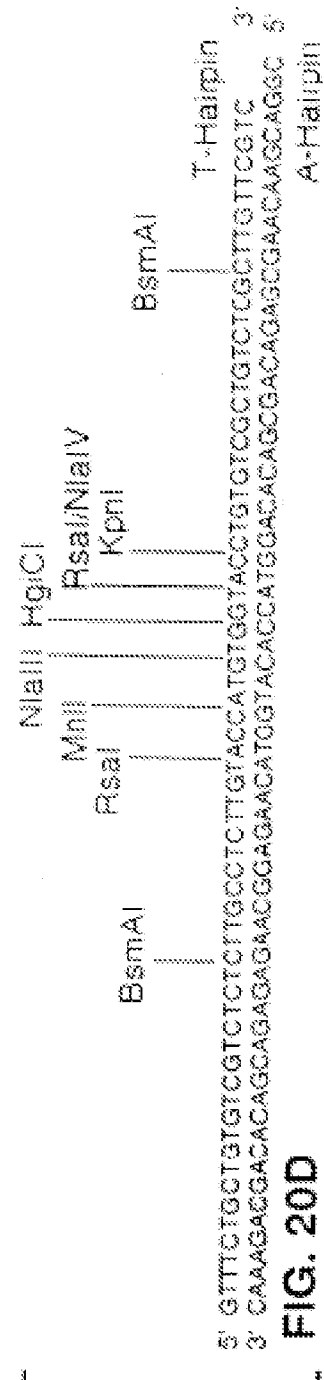


FIG. 20D



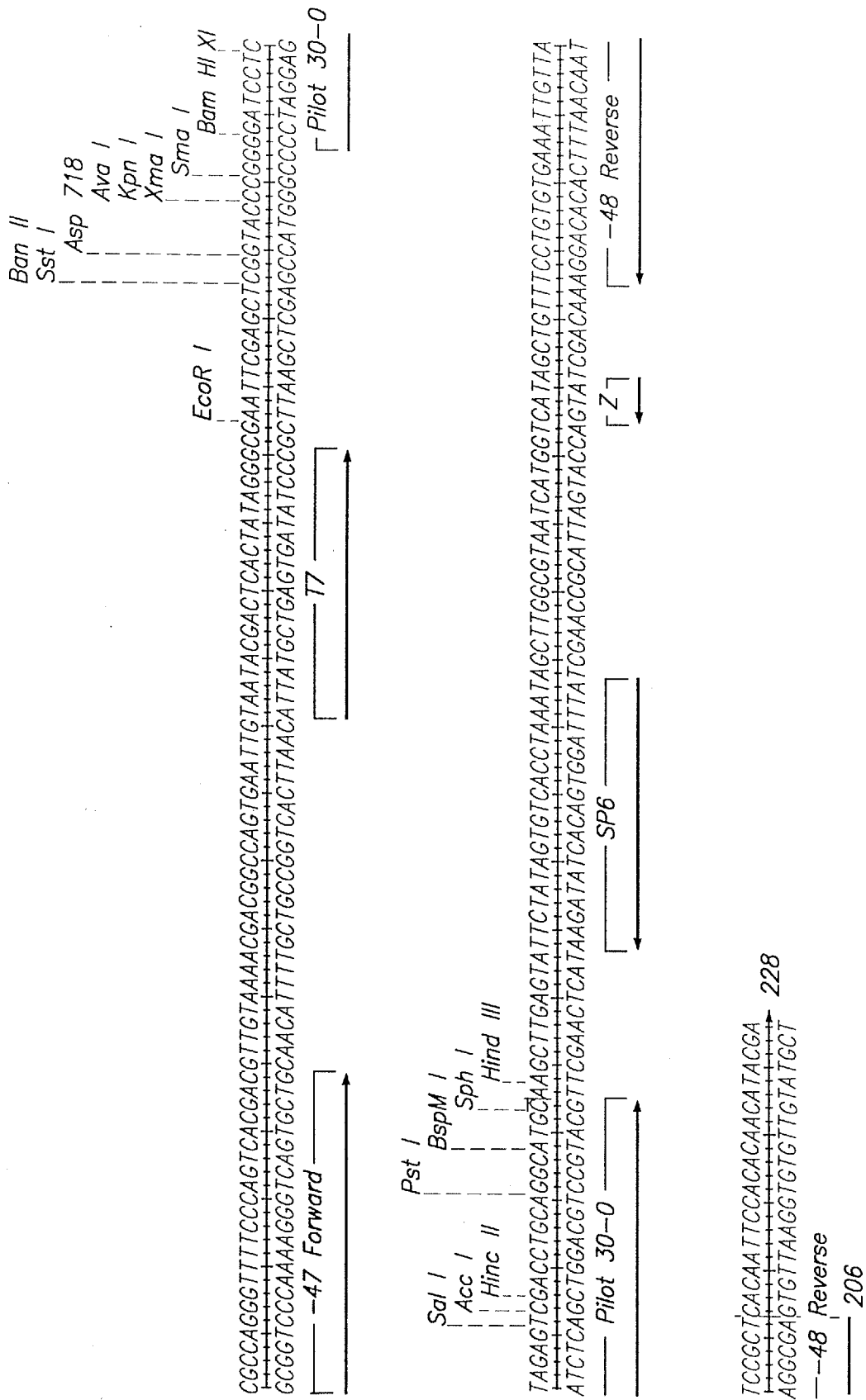


FIGURE 21

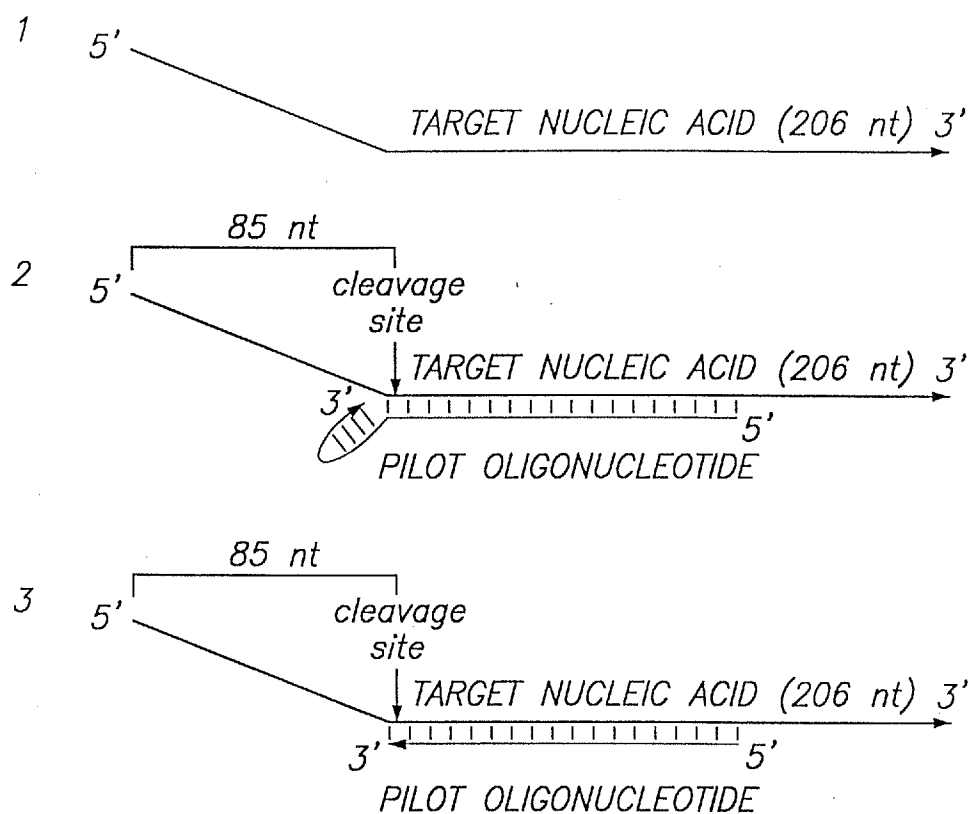


FIGURE 22 A

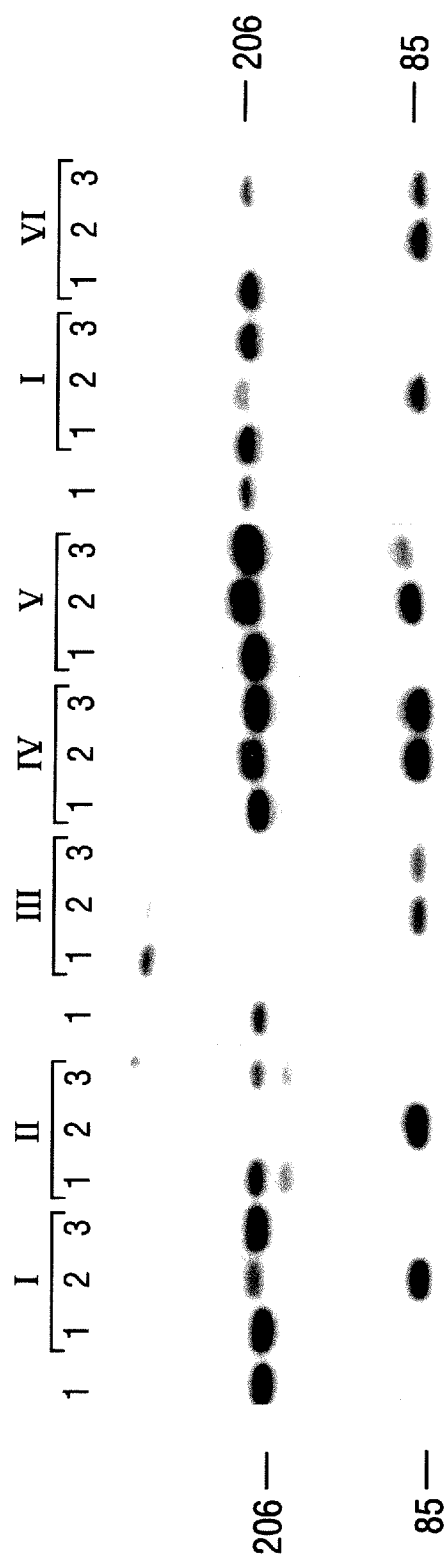
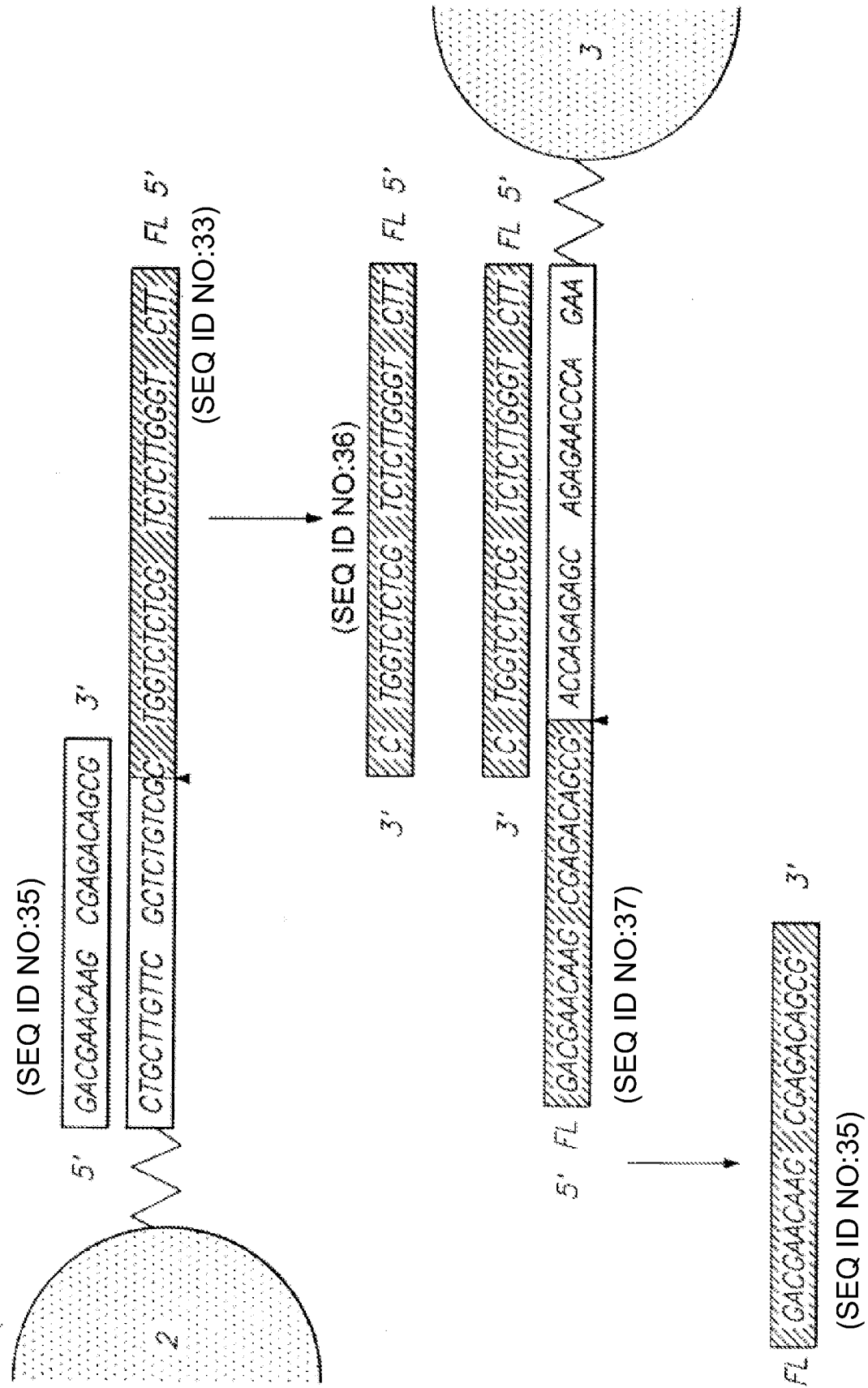


FIG. 22B

FIGURE 23



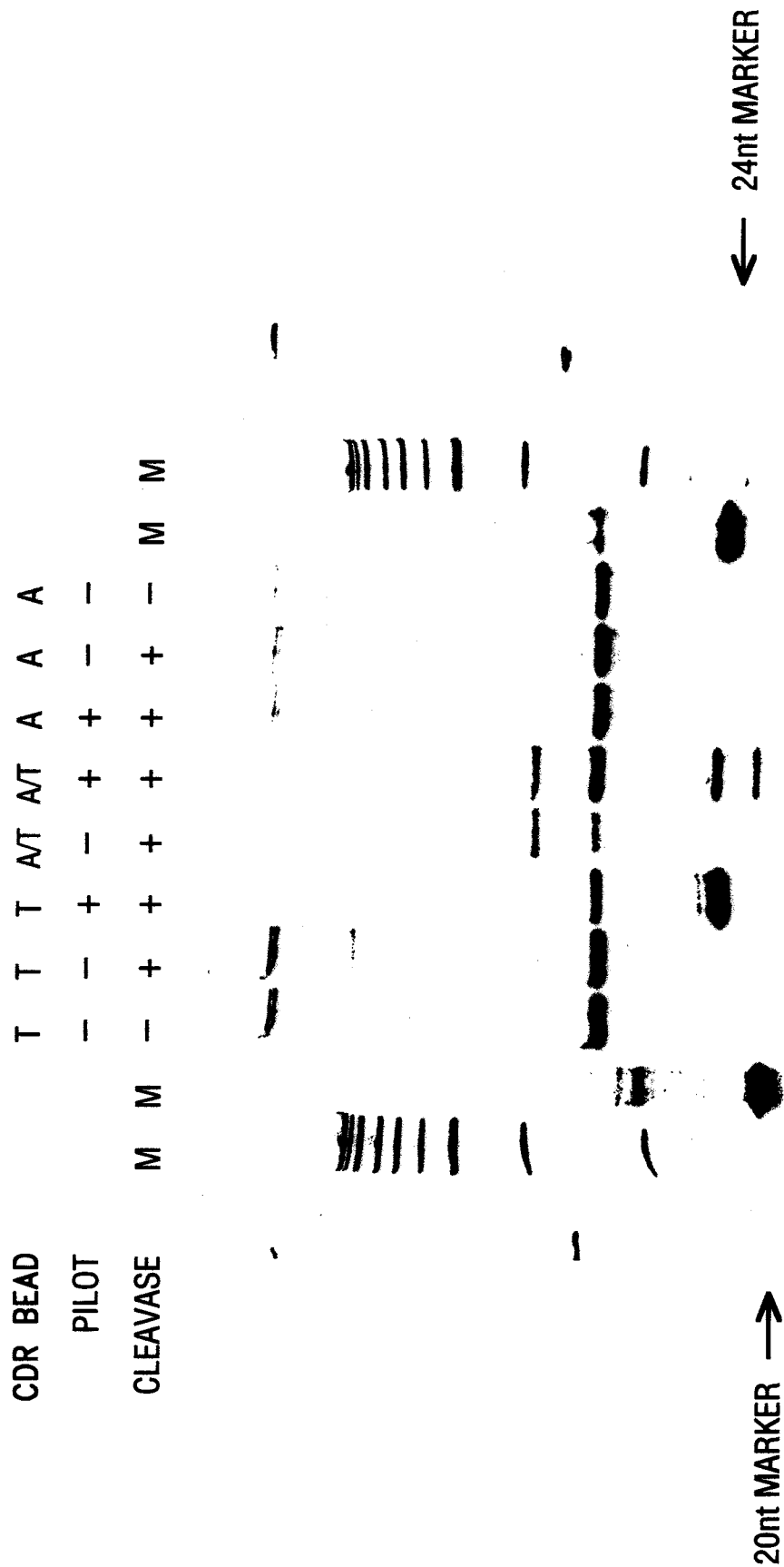


FIG. 24

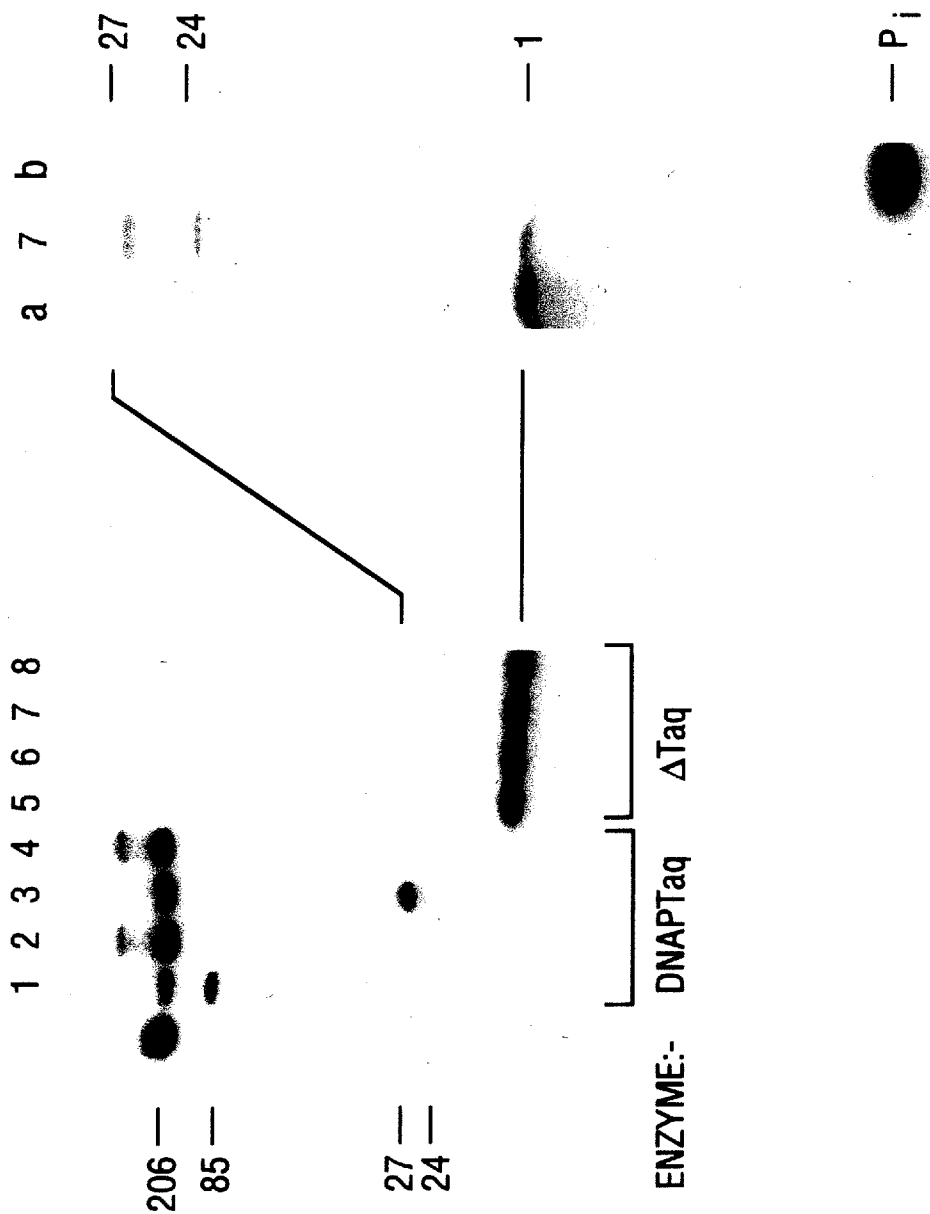


FIG. 25A

FIG. 25B

FIG. 26A



FIG. 26B



\* = 32p



— 206

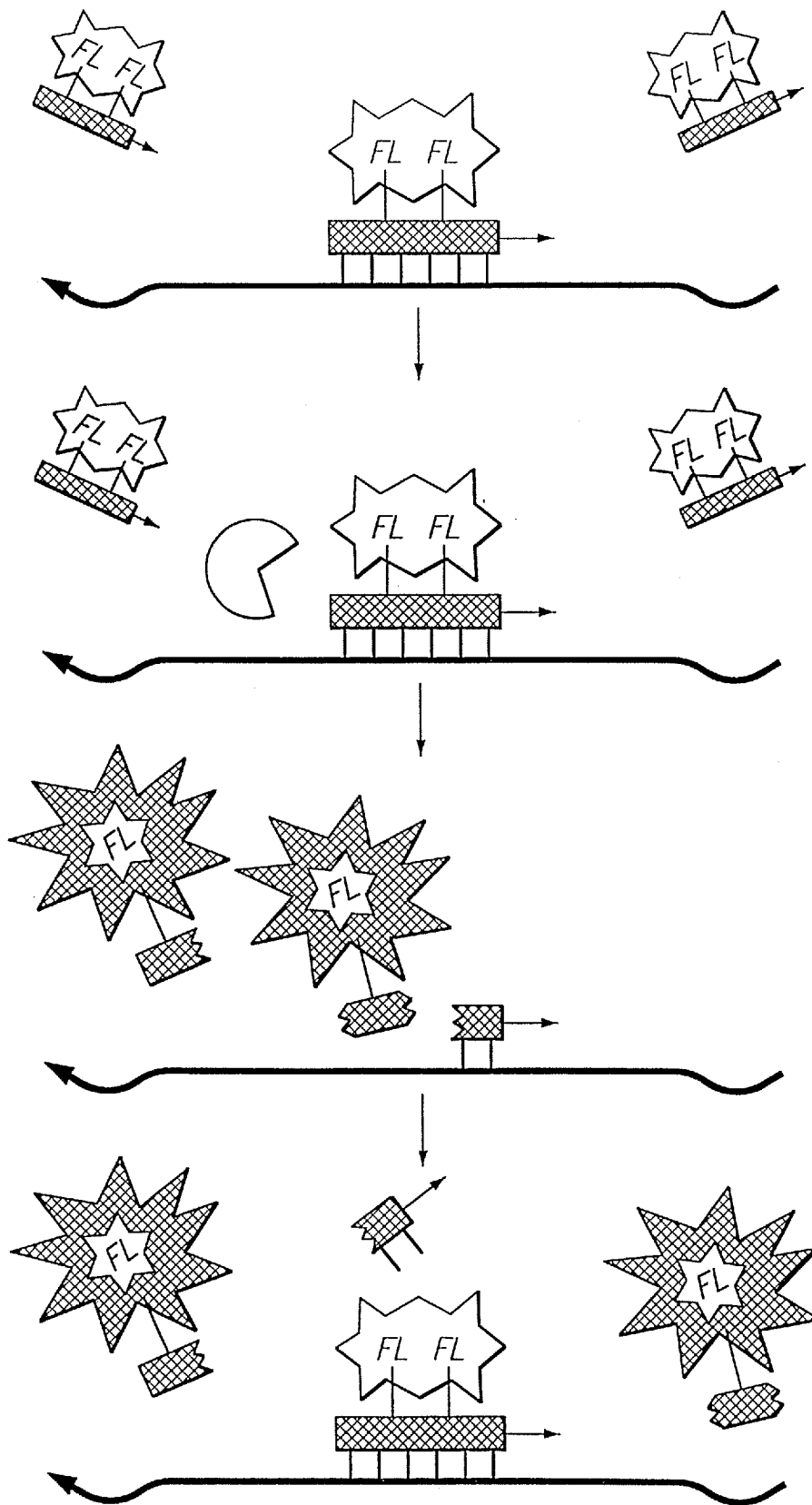


FIGURE 27



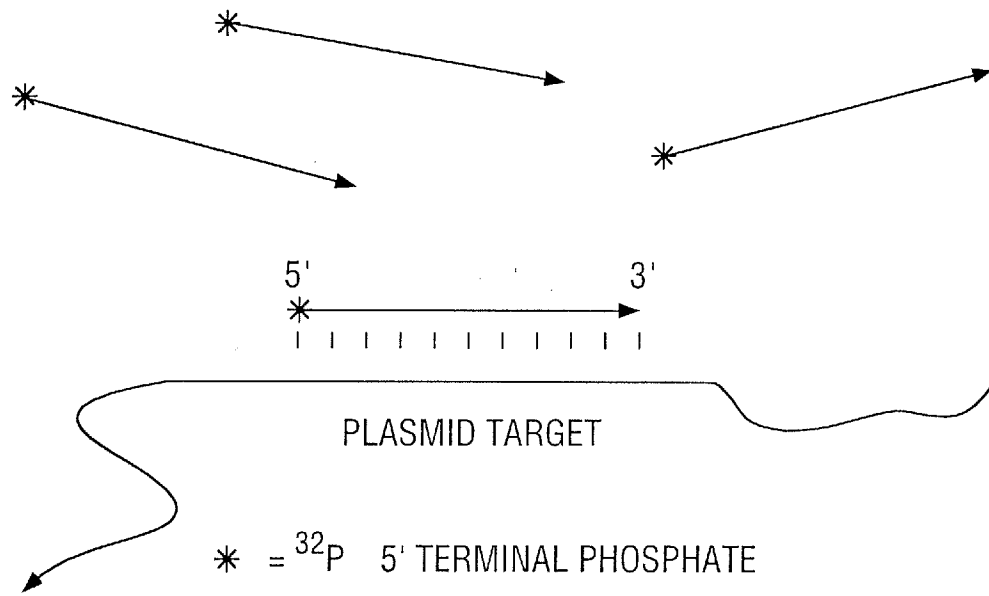
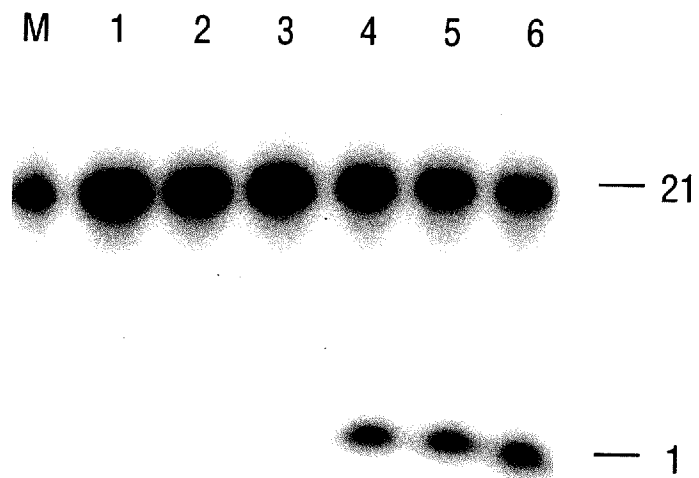


FIGURE 28 A



**FIG. 28B**

FIGURE 29

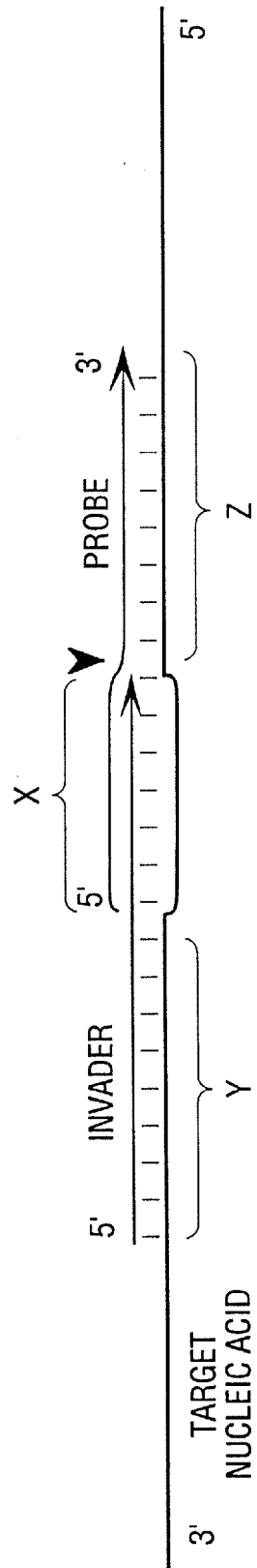


FIGURE 30

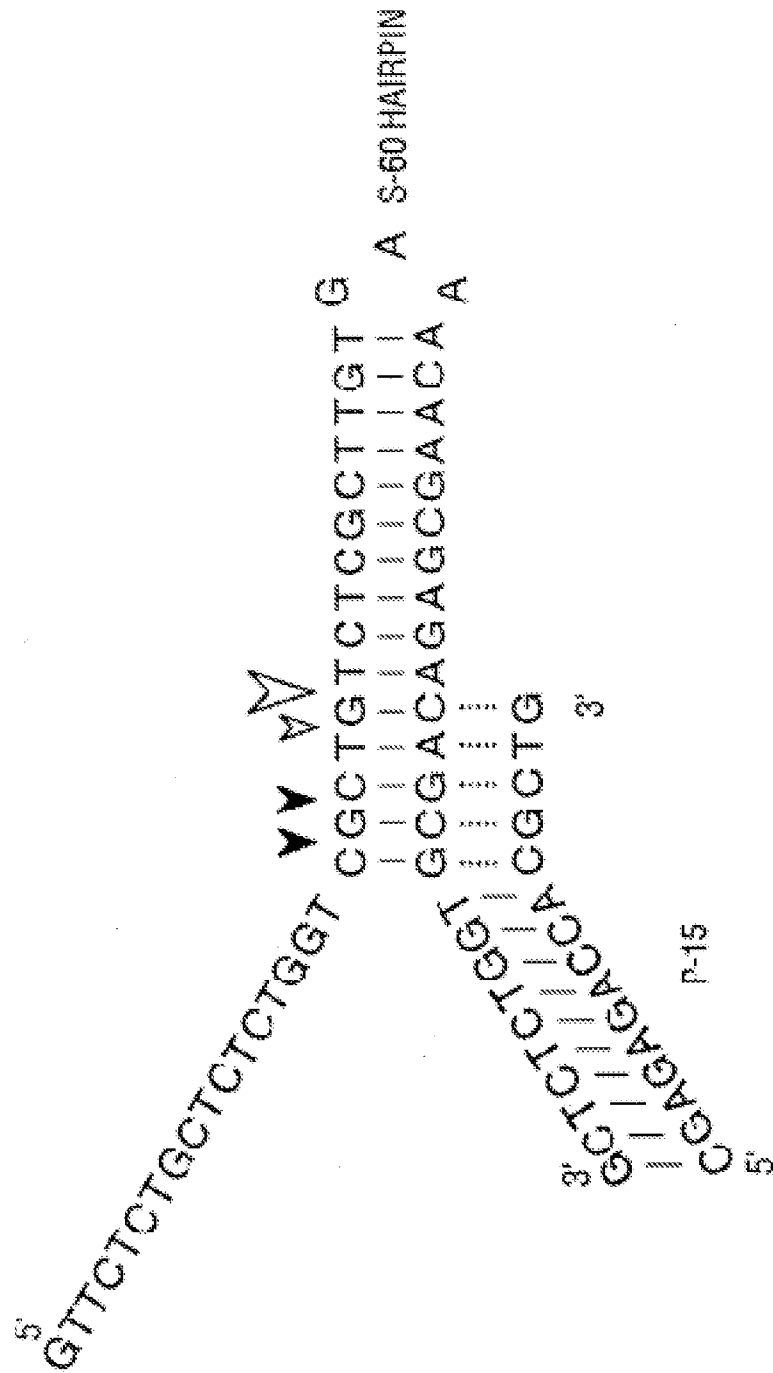


FIGURE 31

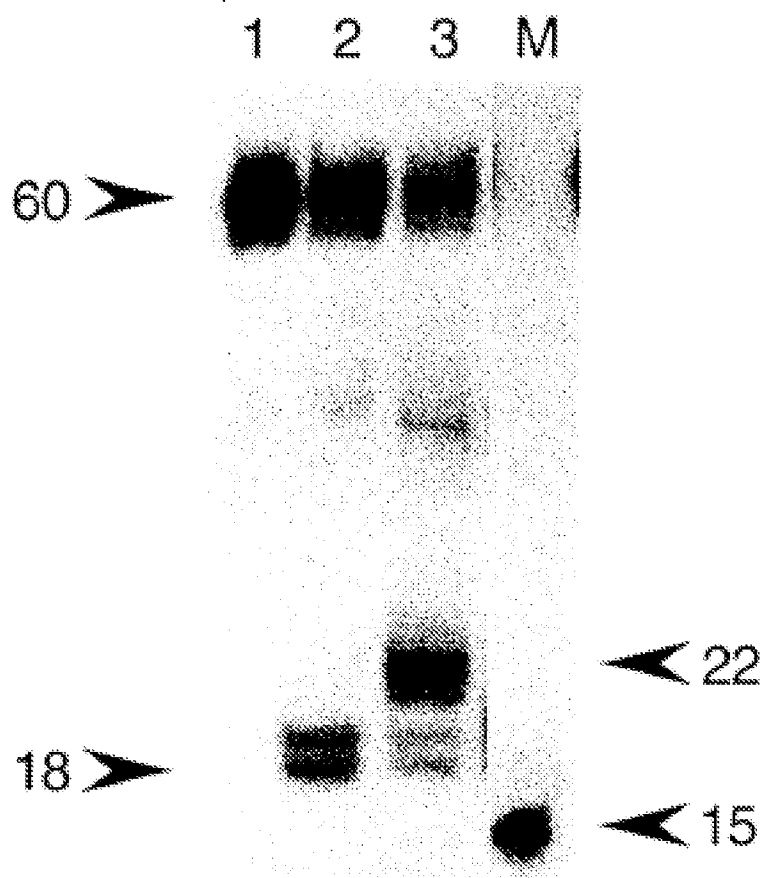


FIGURE 32

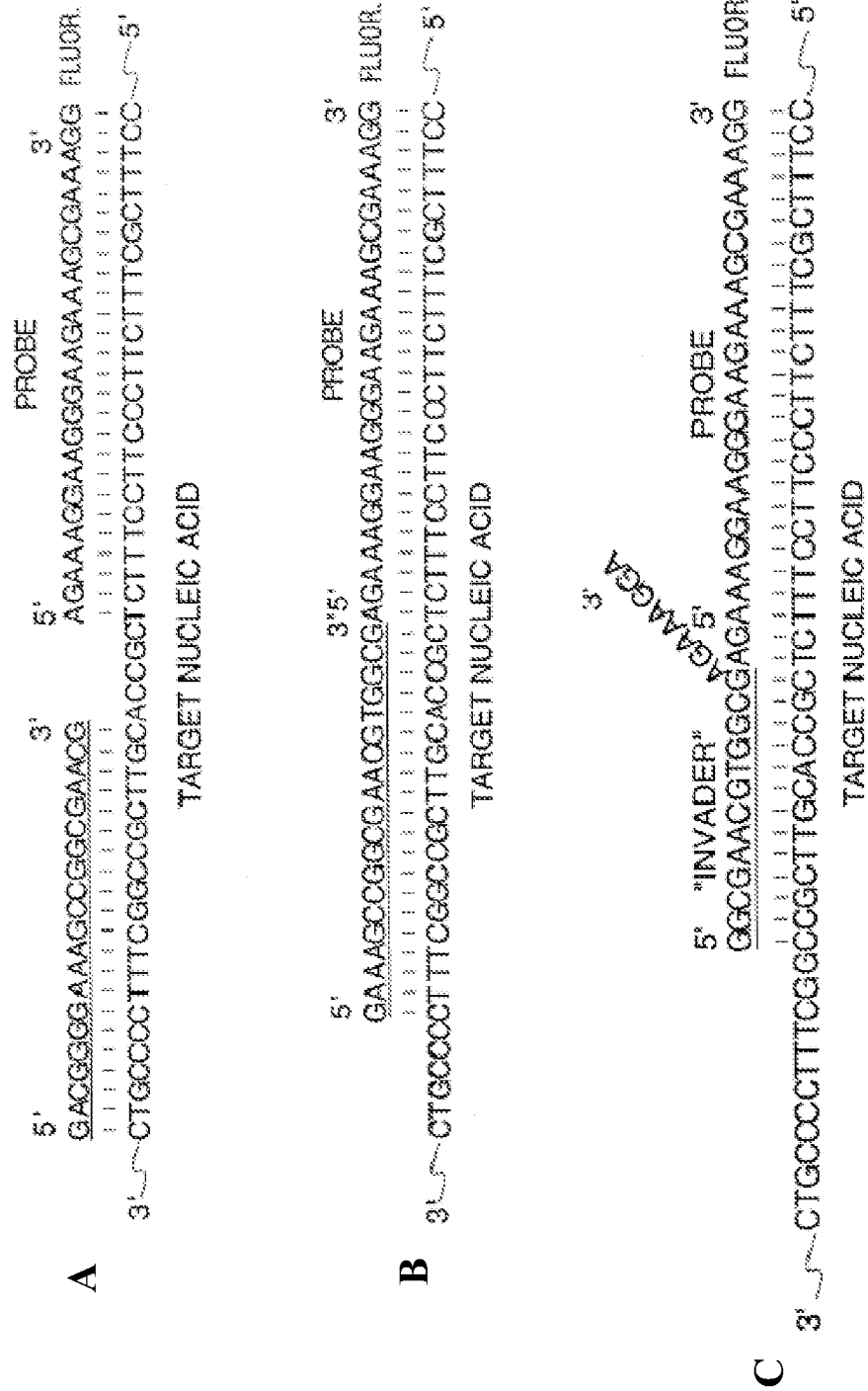


FIGURE 33

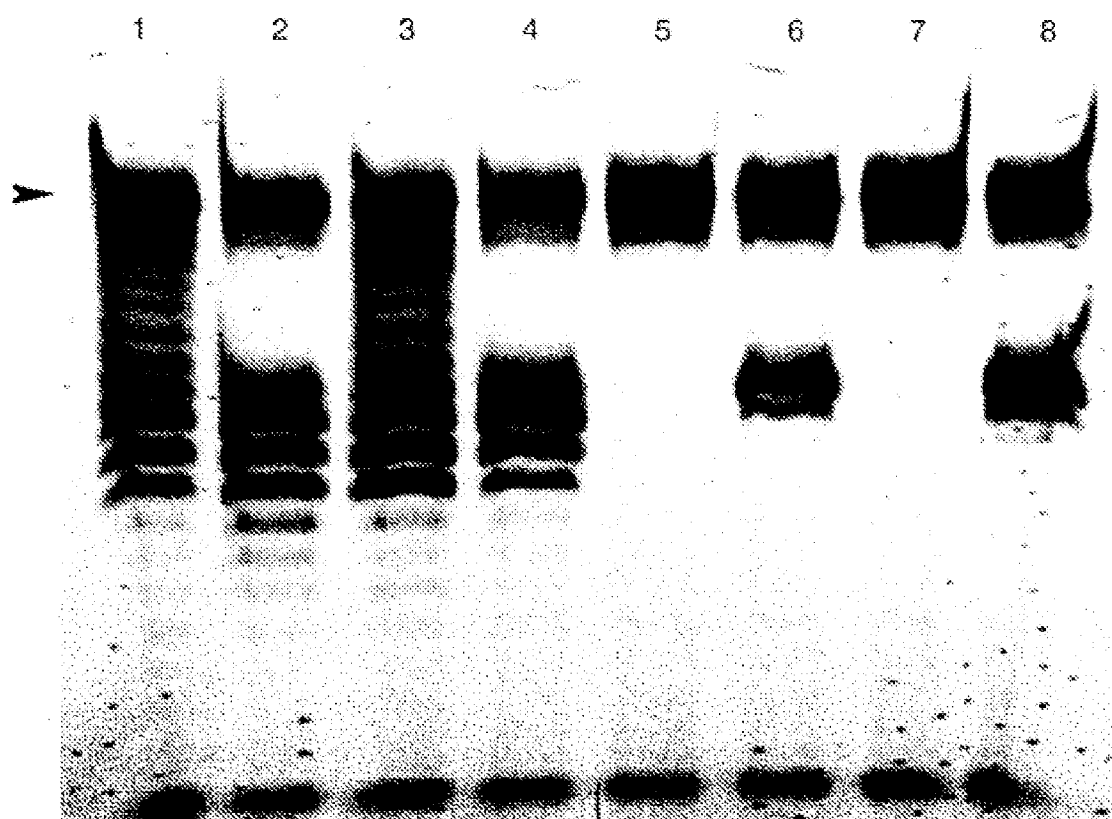


FIGURE 34

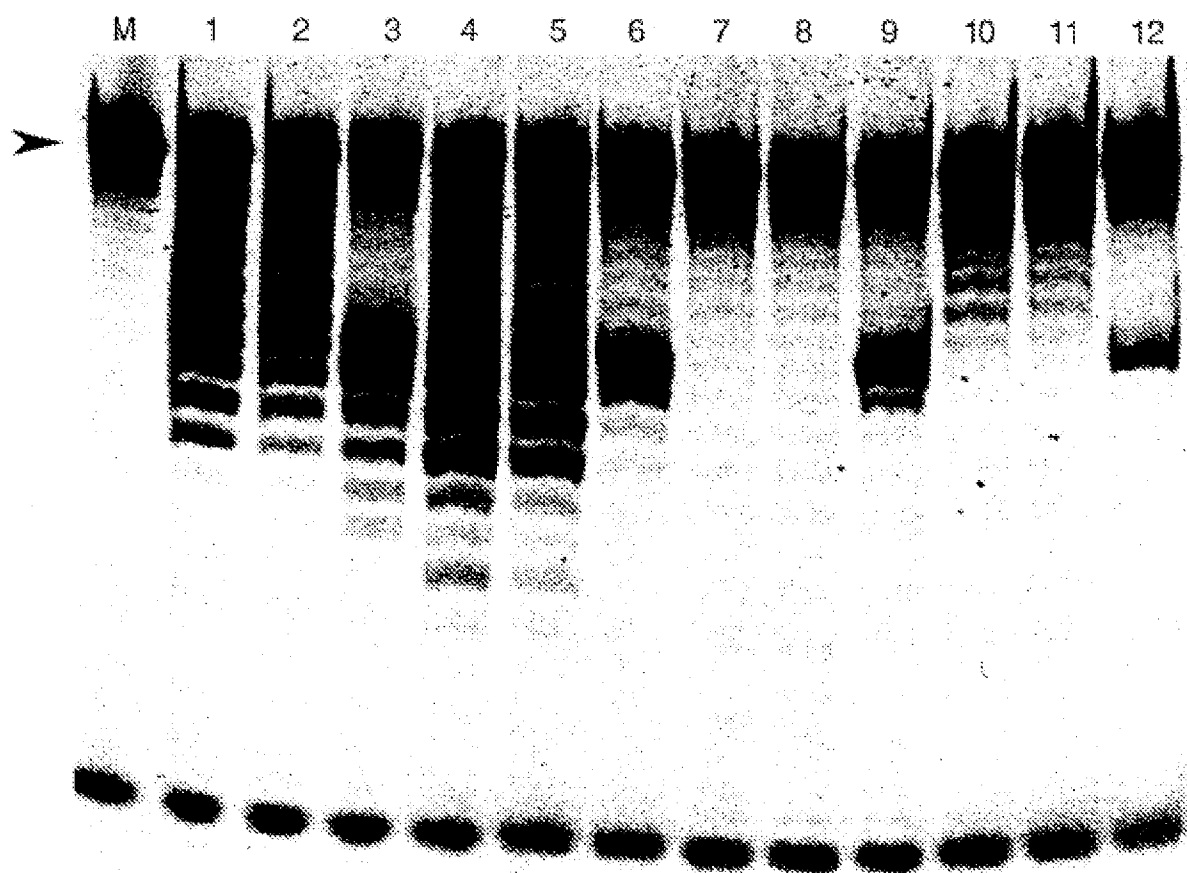




FIGURE 35

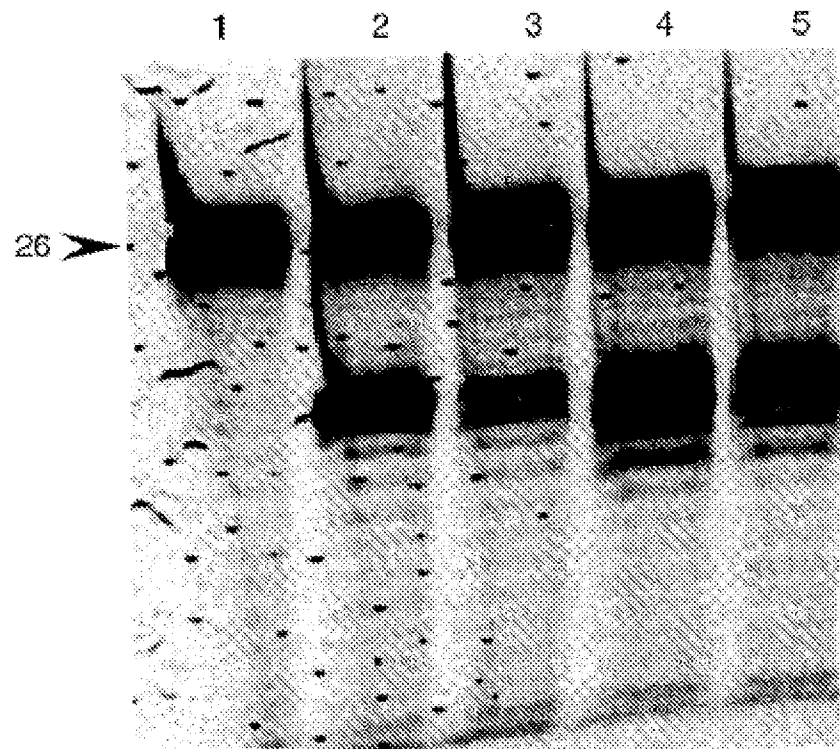


FIGURE 36

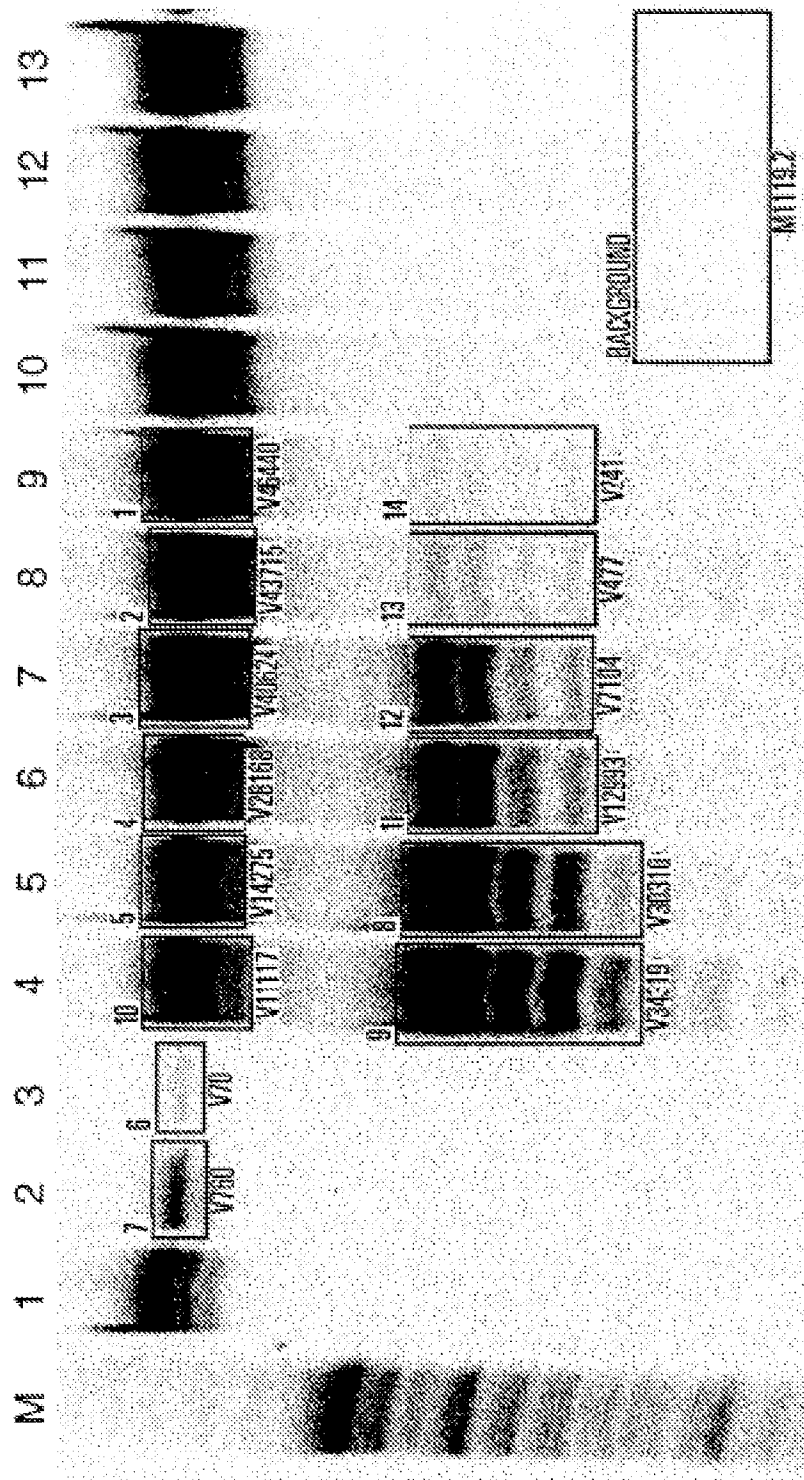


FIGURE 37

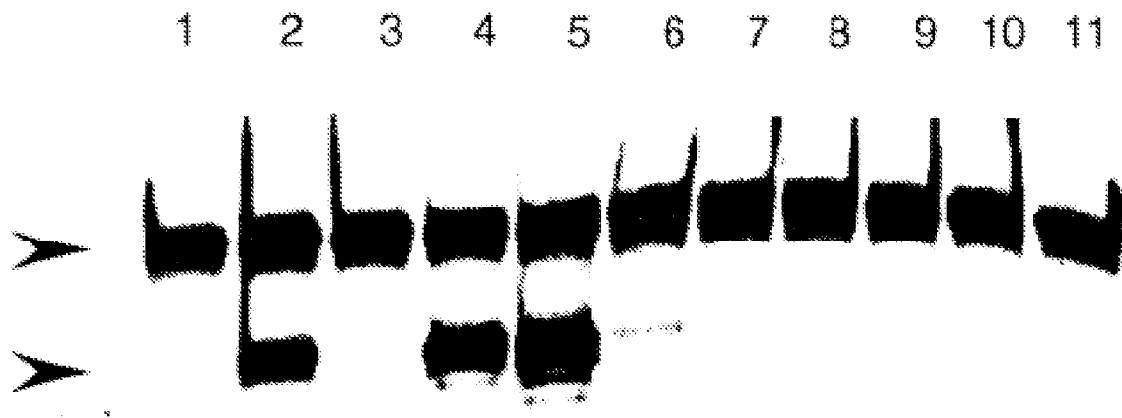


FIGURE 38

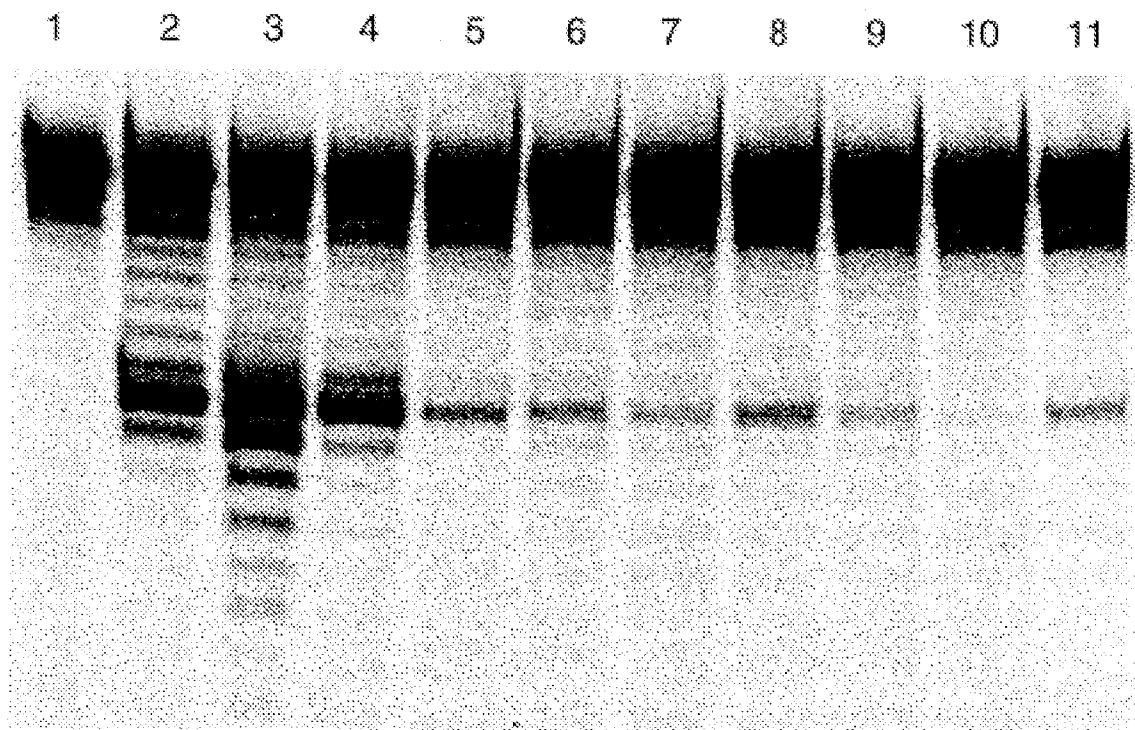


FIGURE 39

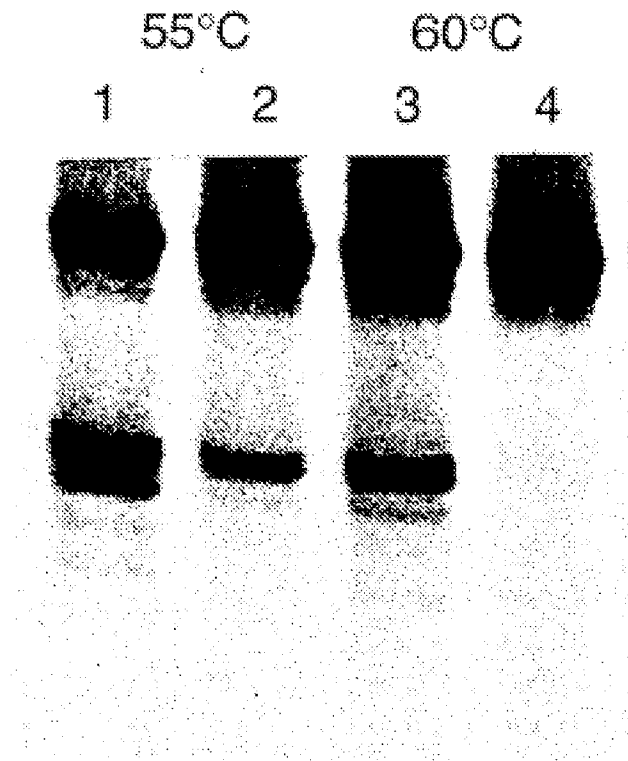


FIGURE 40

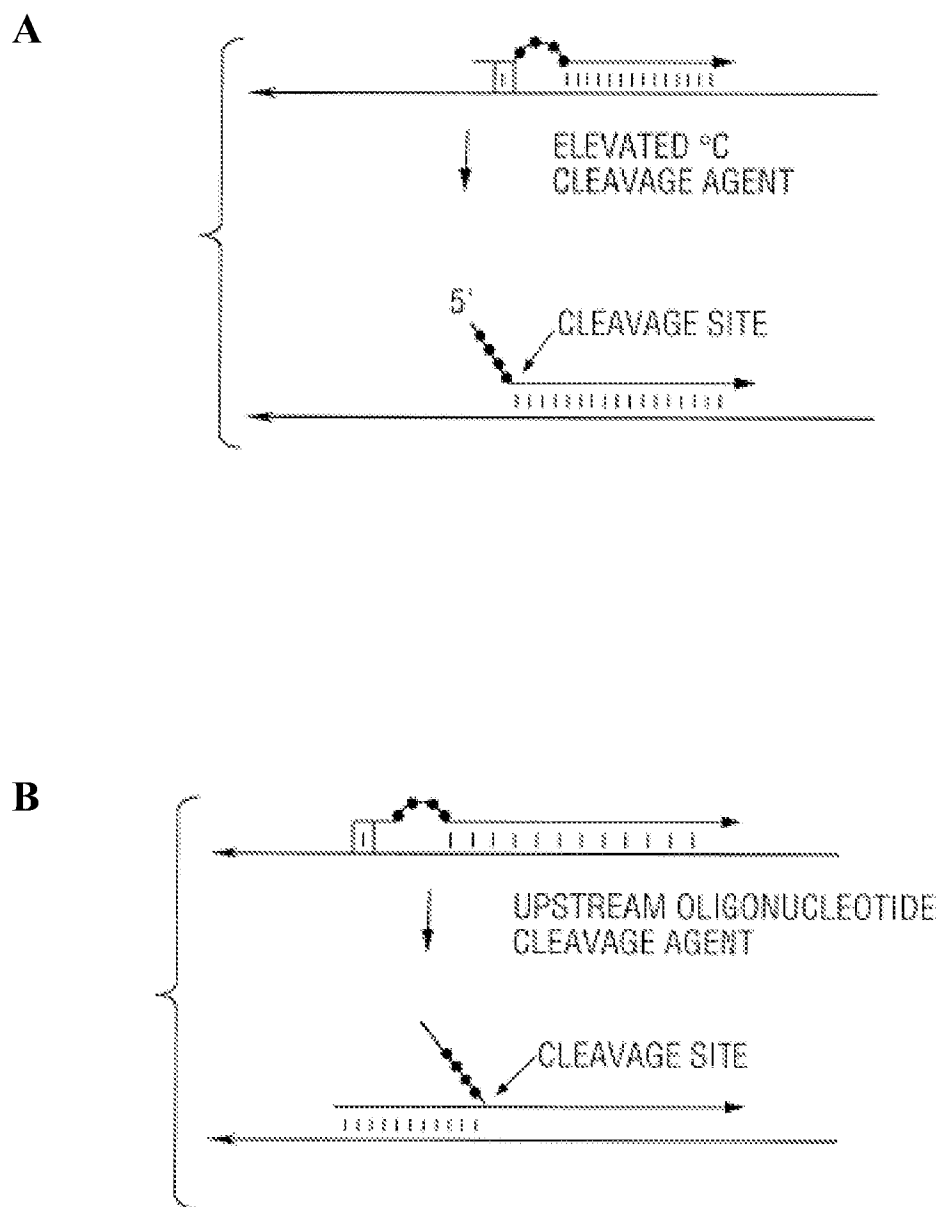


FIGURE 41

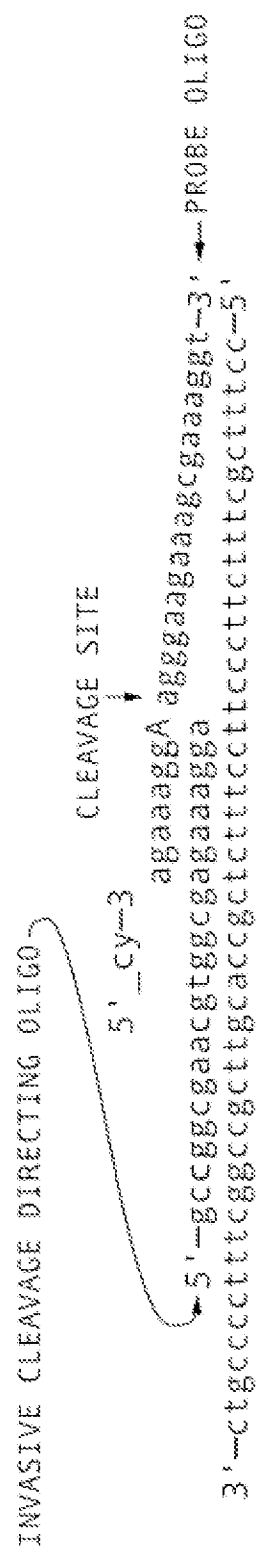
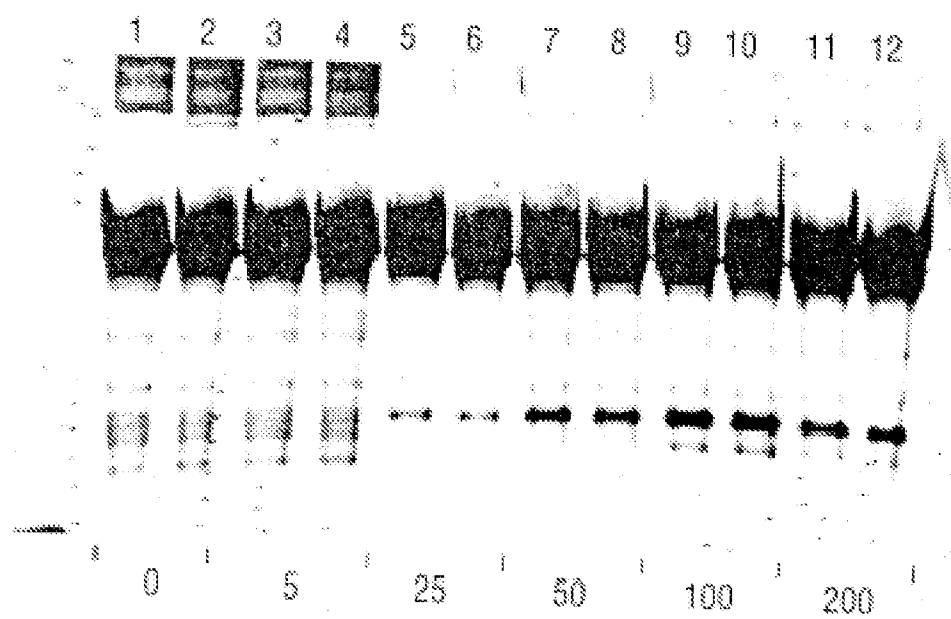
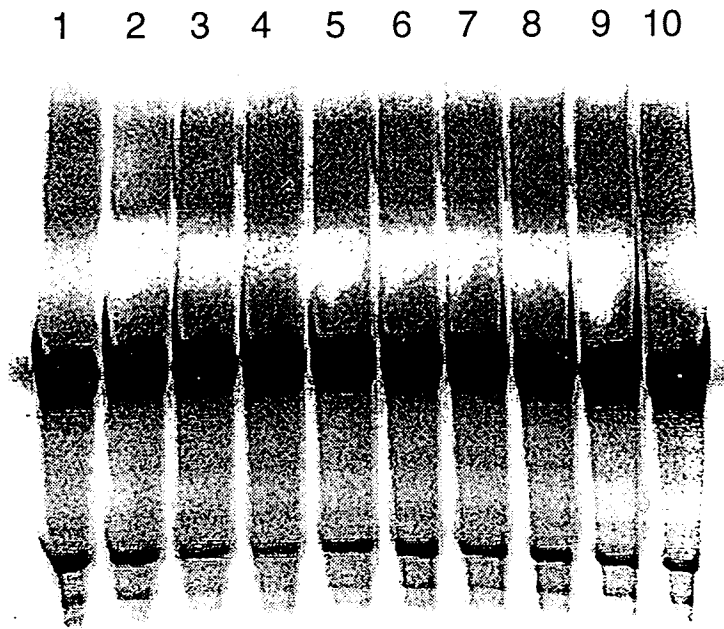


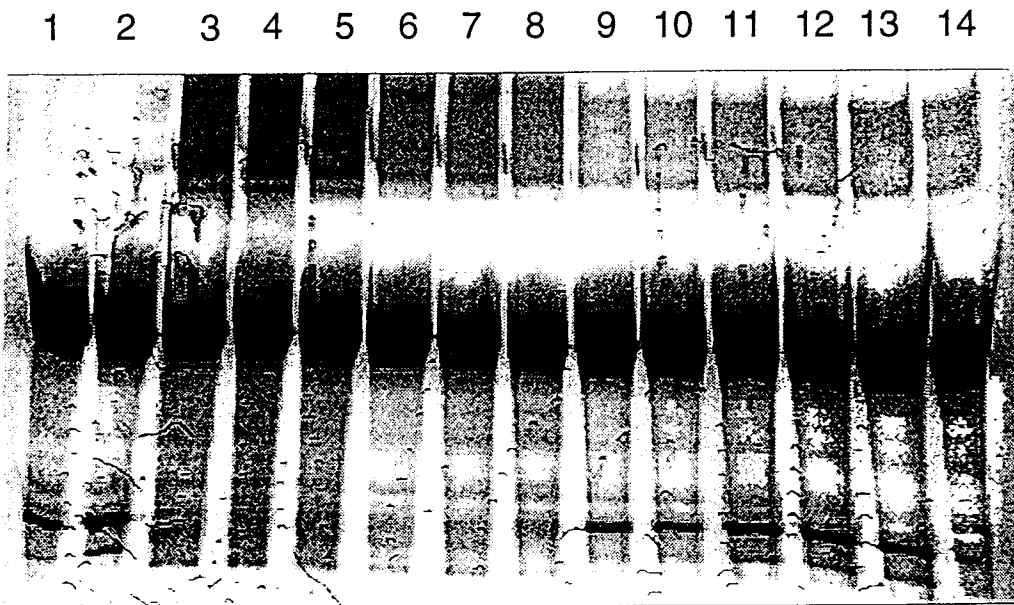
FIGURE 42







**FIG. 43**



**FIG. 44**

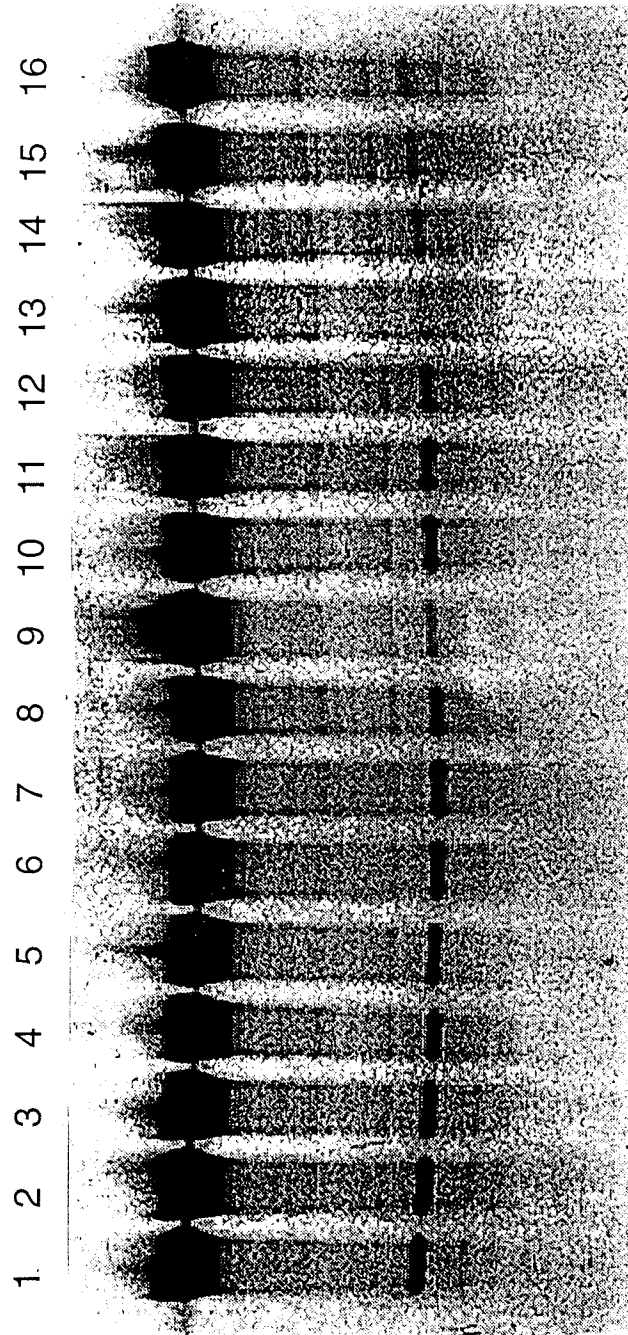
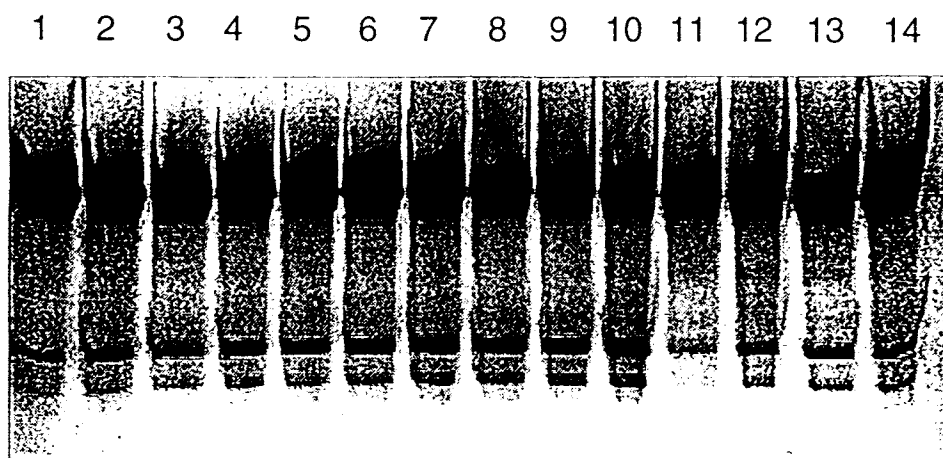


FIG. 45



**FIG. 46**

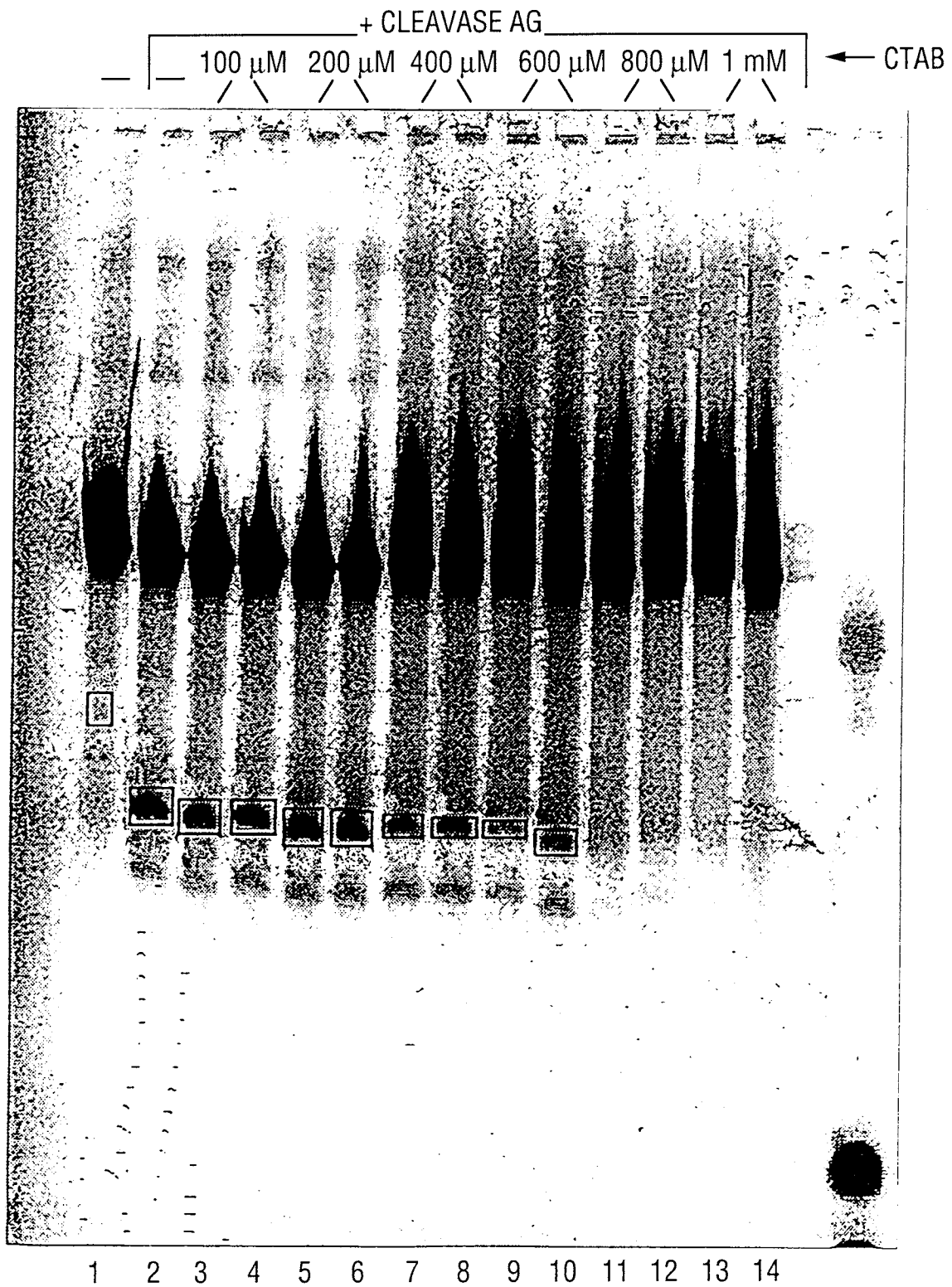
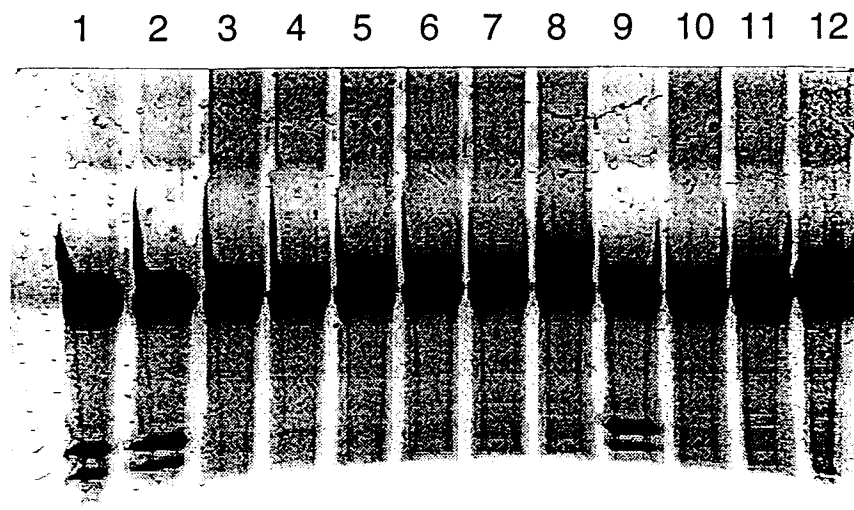
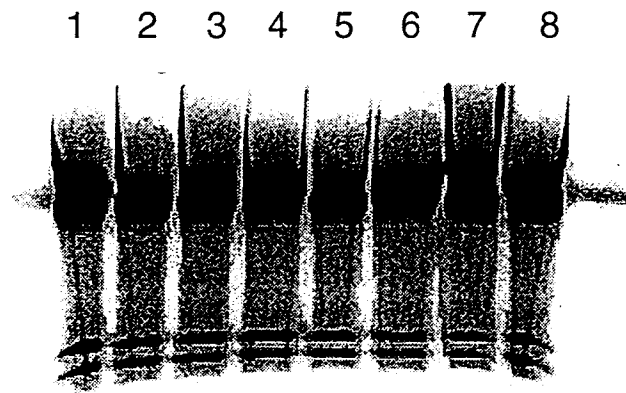


FIG. 47



**FIG. 48**



**FIG. 49**

**FIG. 50**

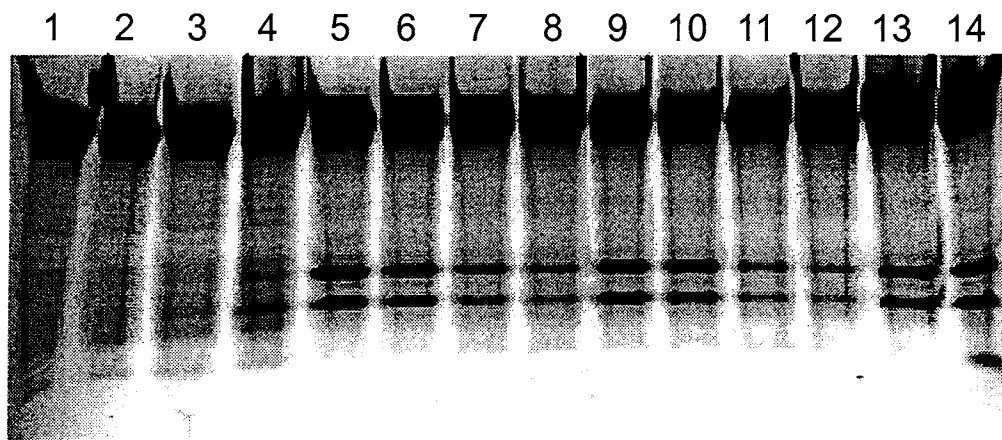




FIGURE 51

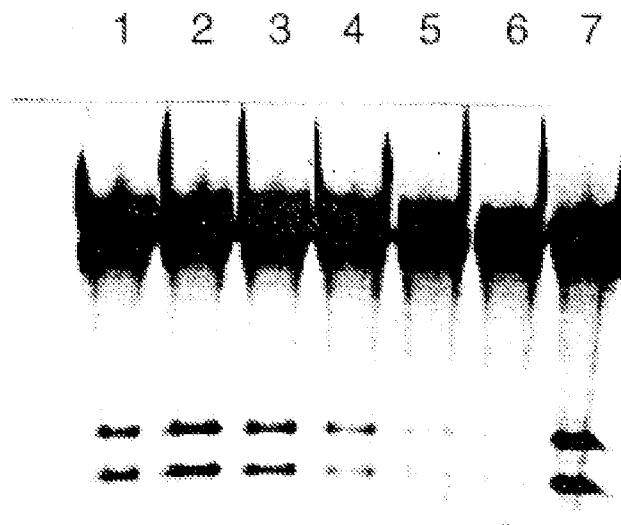


FIGURE 52

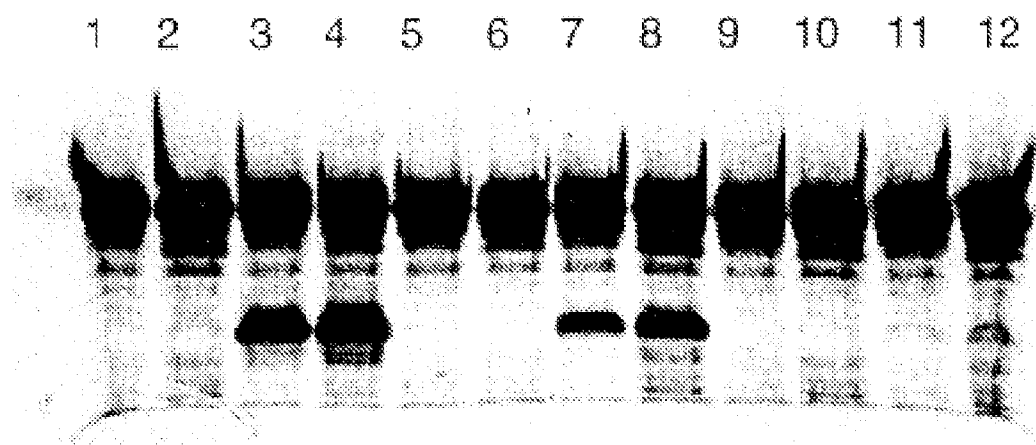


FIGURE 53

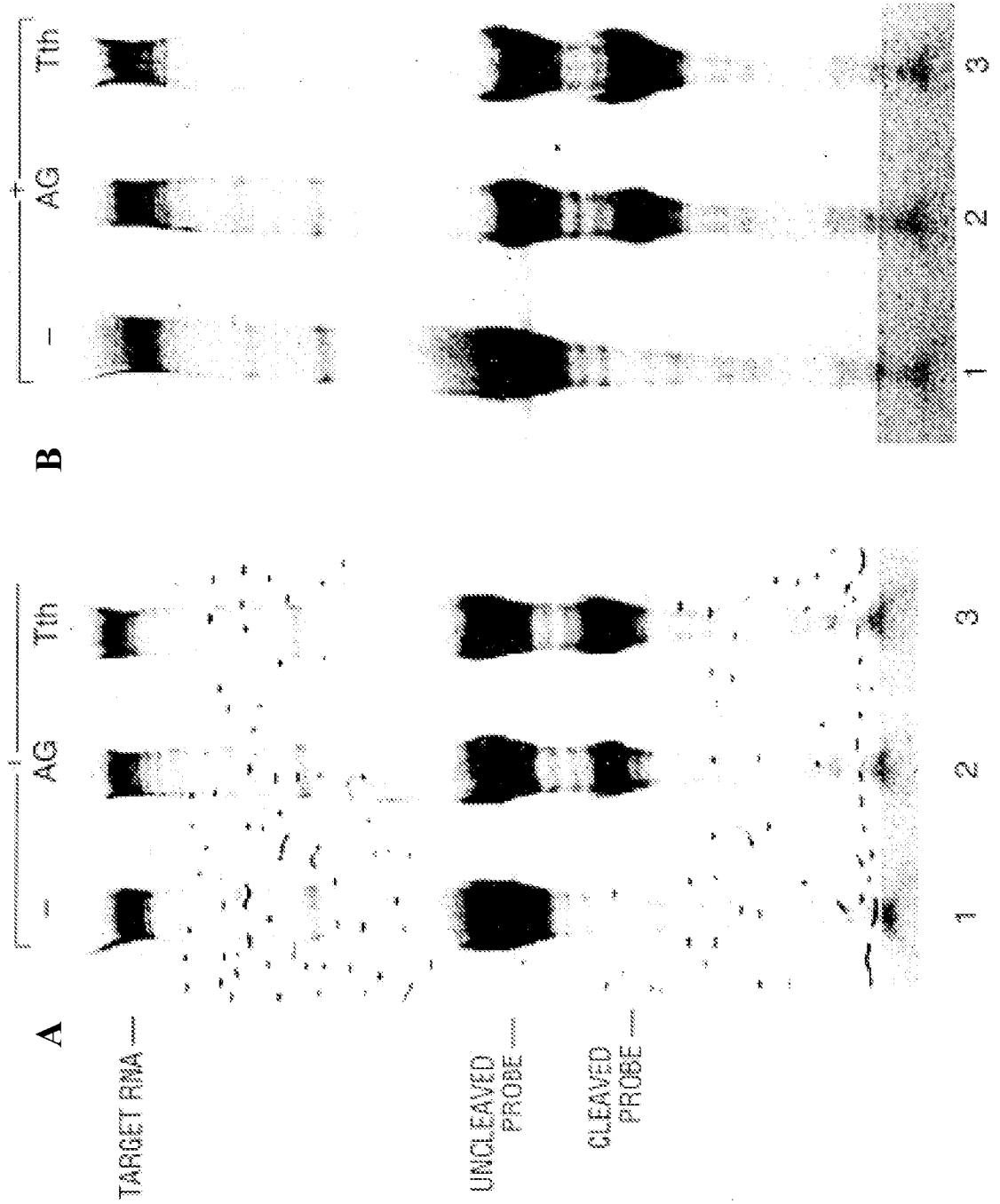
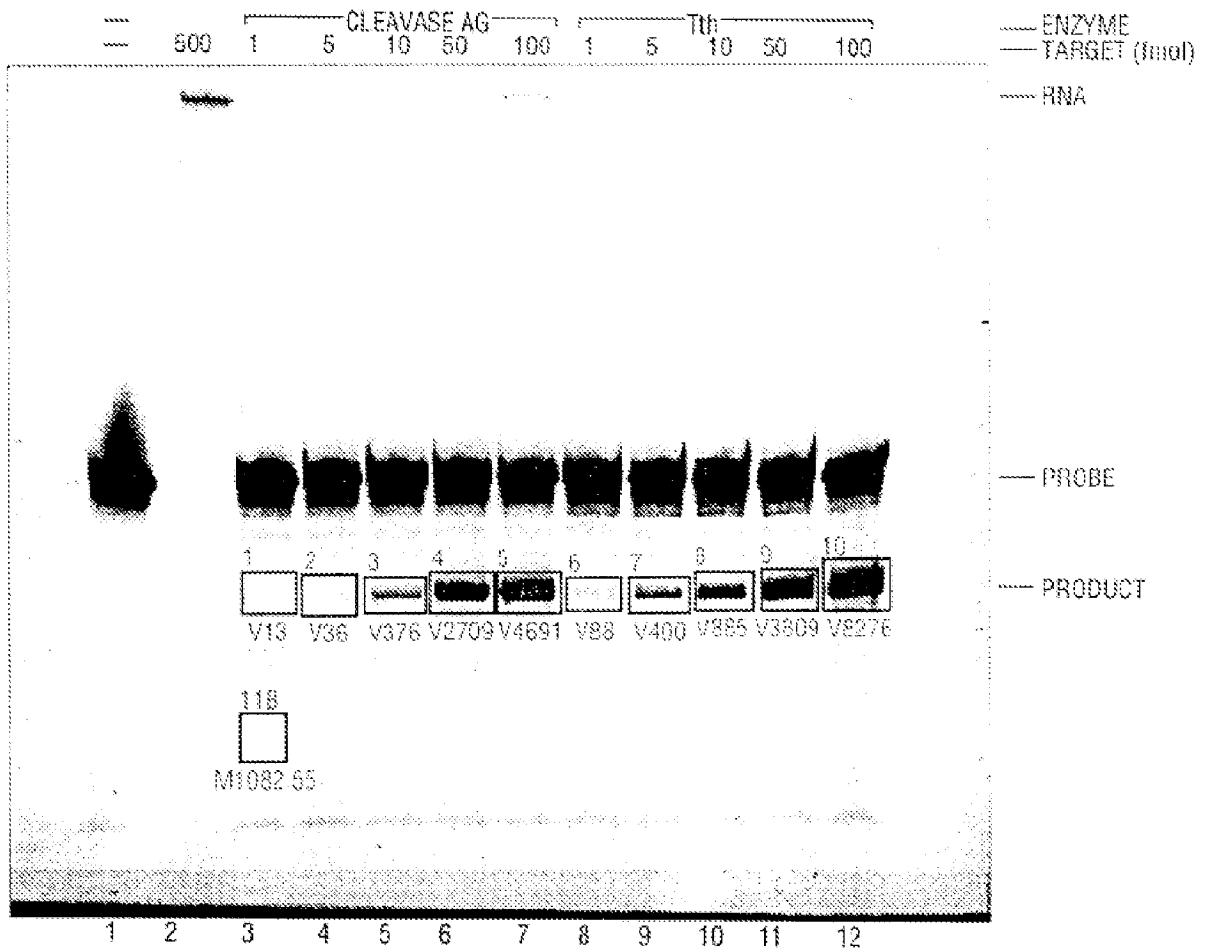
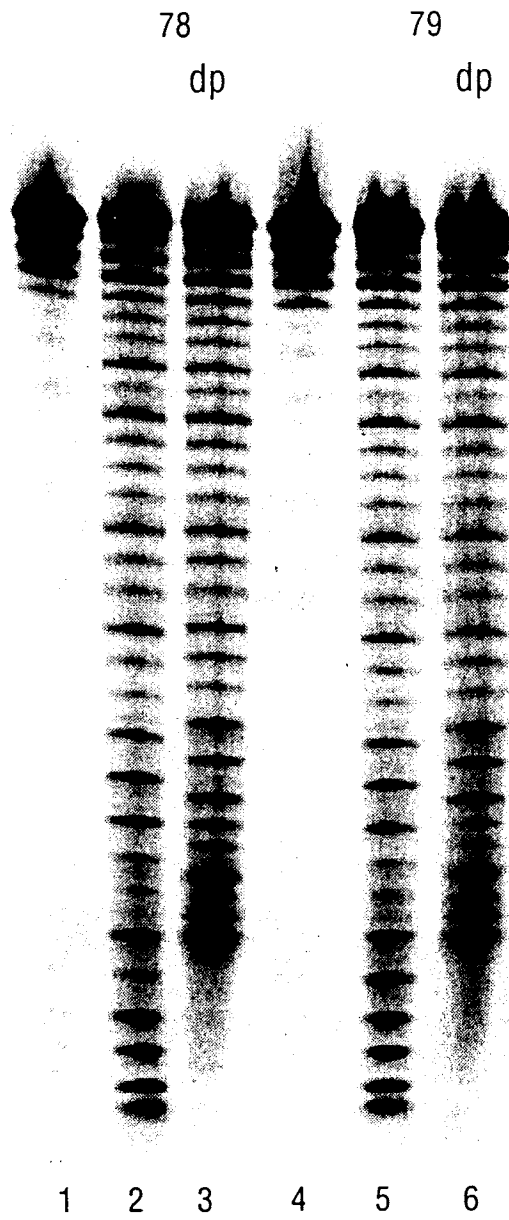


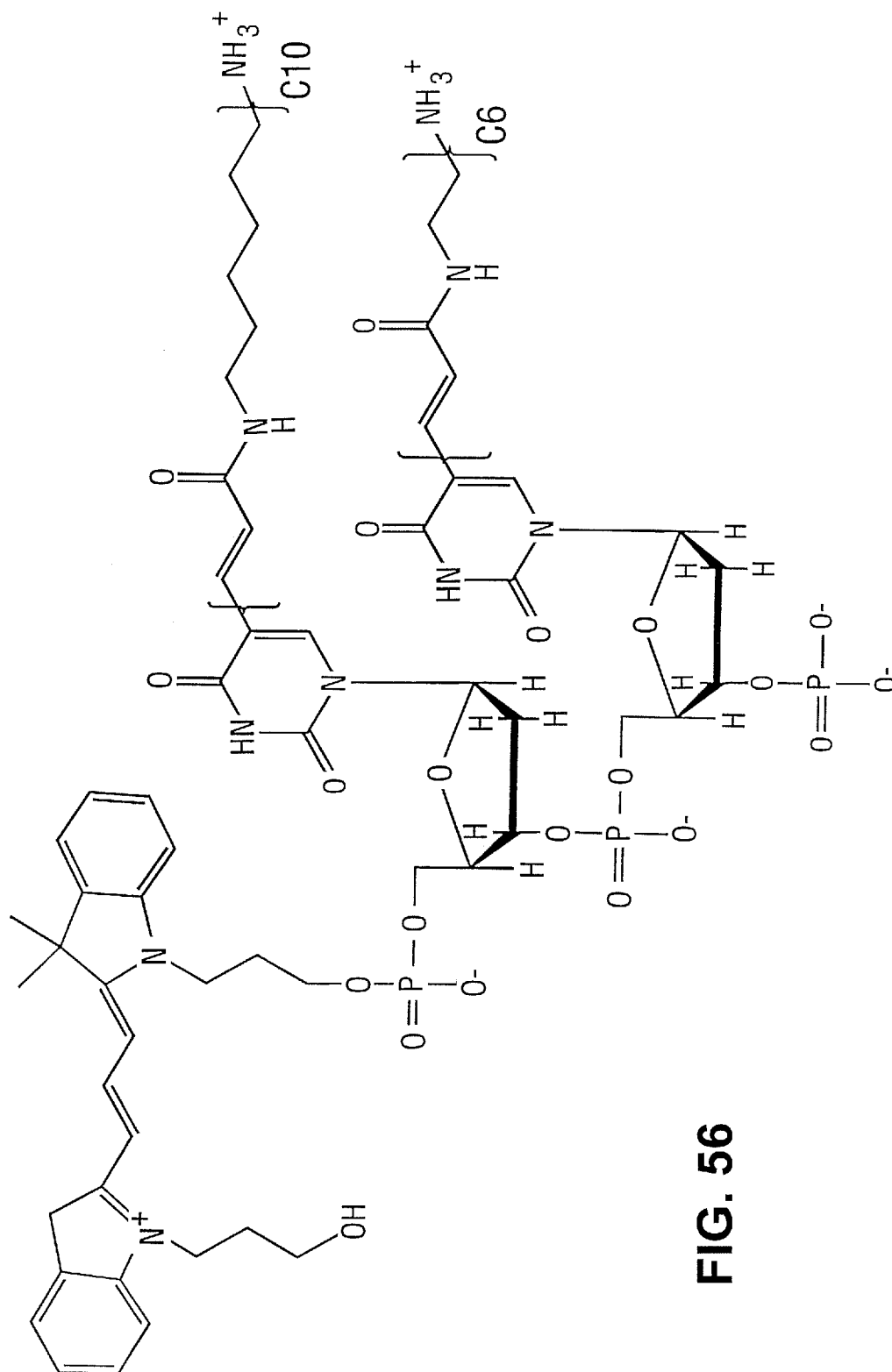
FIGURE 54





**FIG. 55**

70 (C10 amino T's)  
74 (C6 amino T's)



**FIG. 56**

75

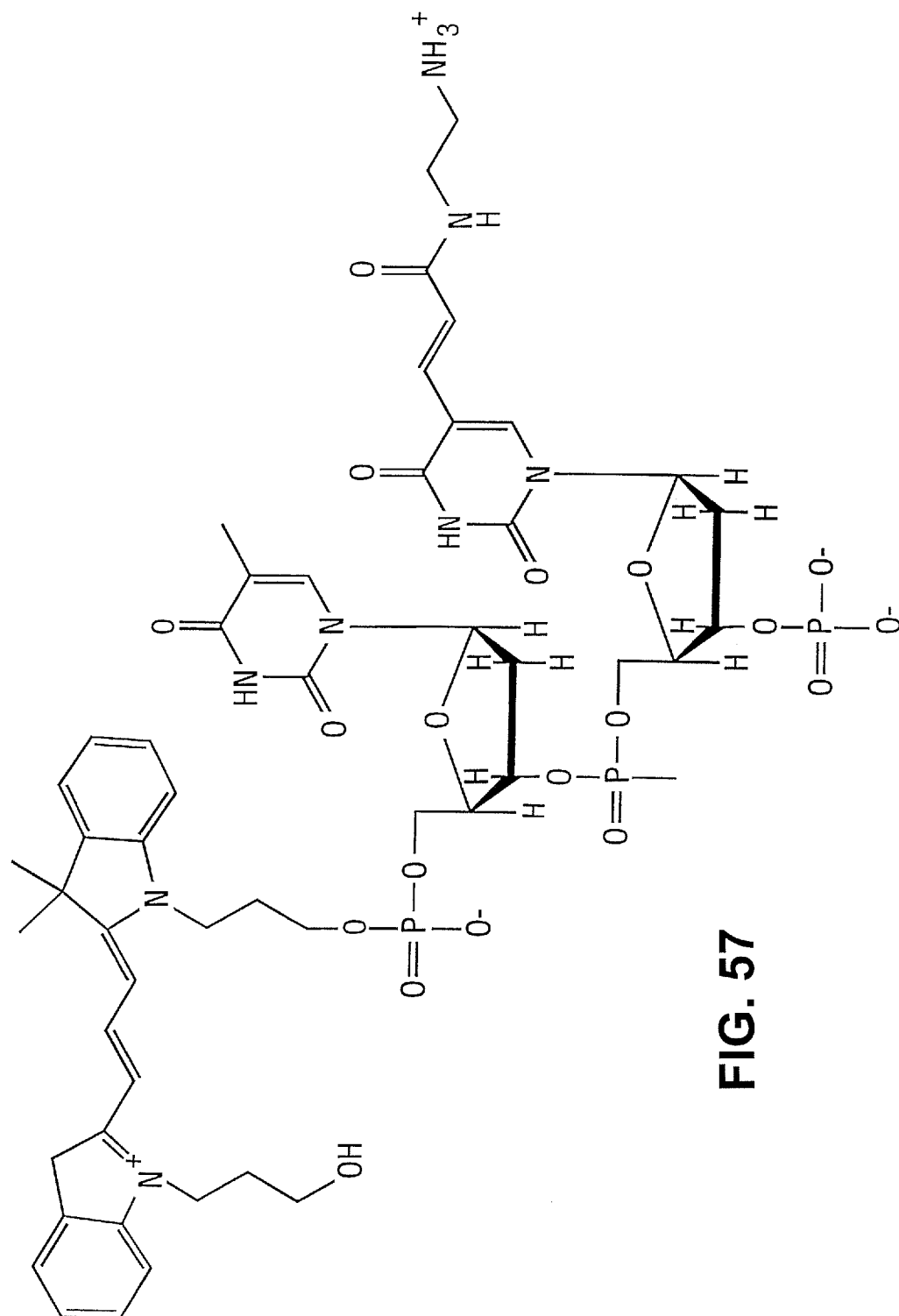
**FIG. 57**

FIGURE 58

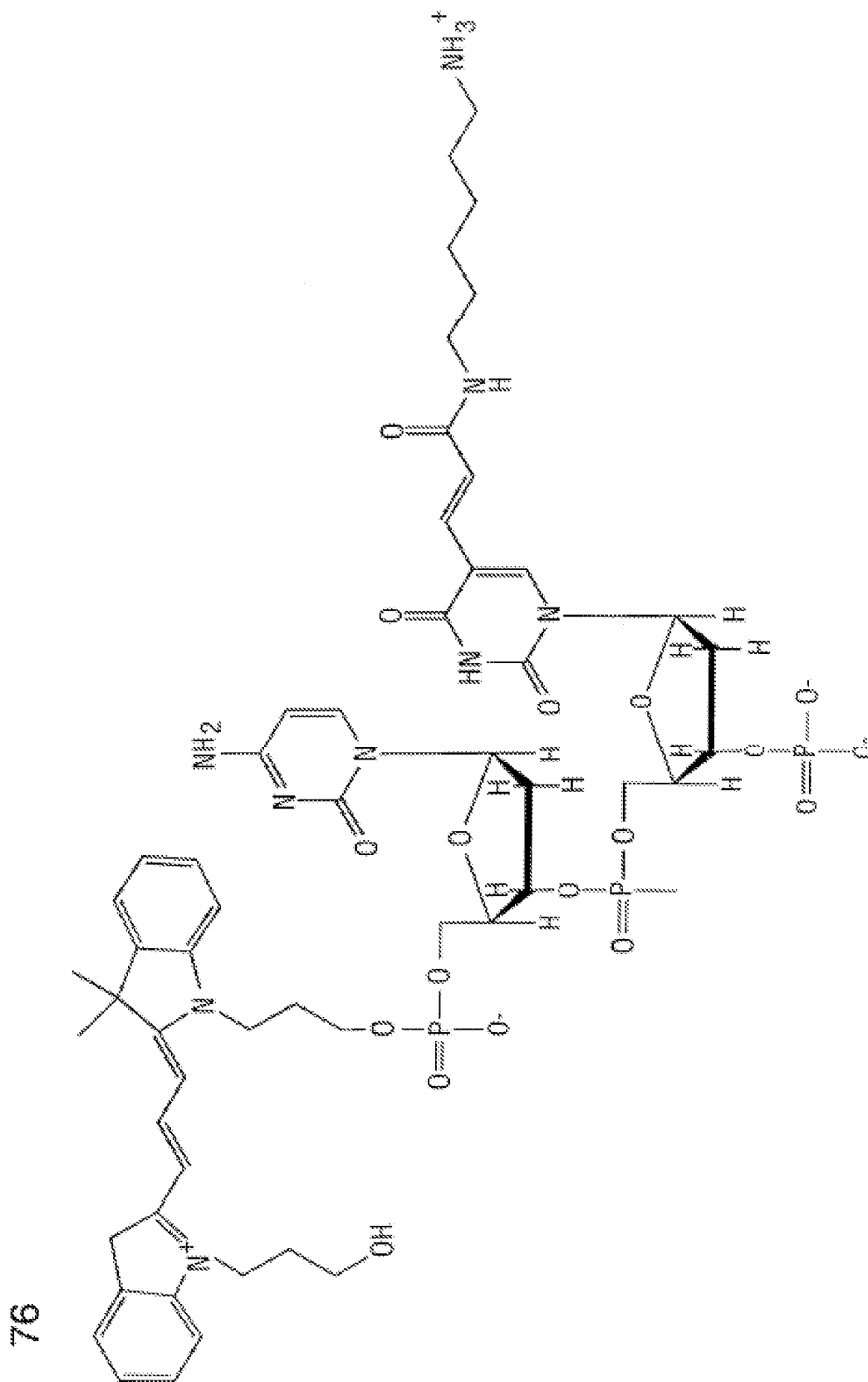




FIGURE 59

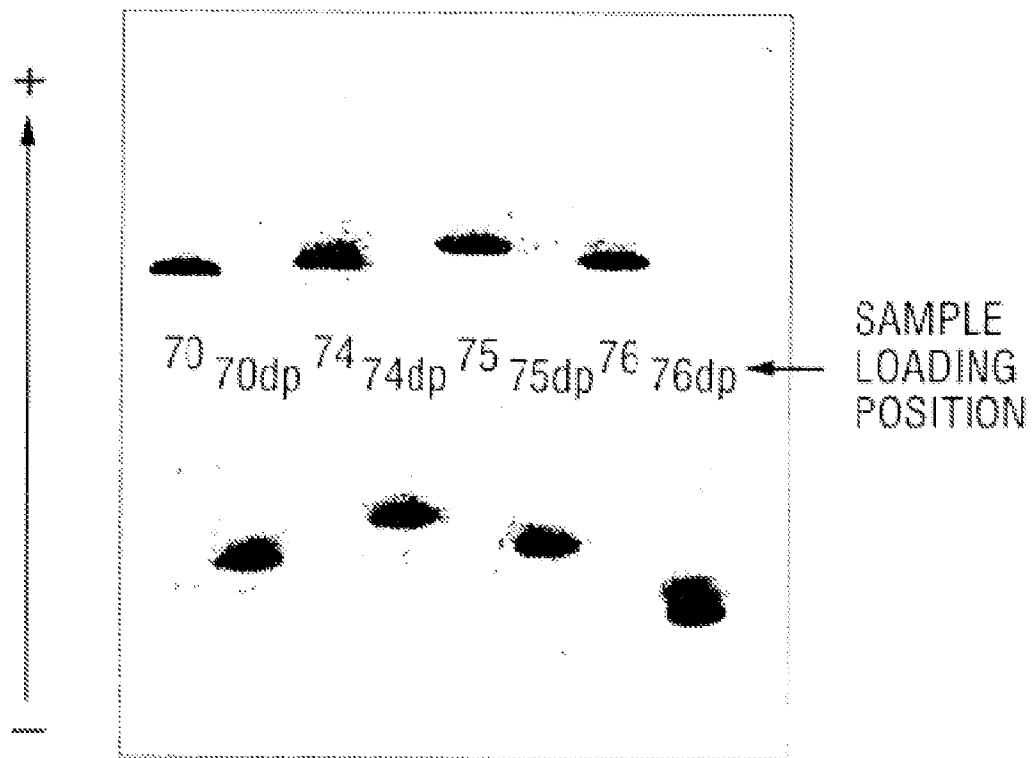


FIGURE 60

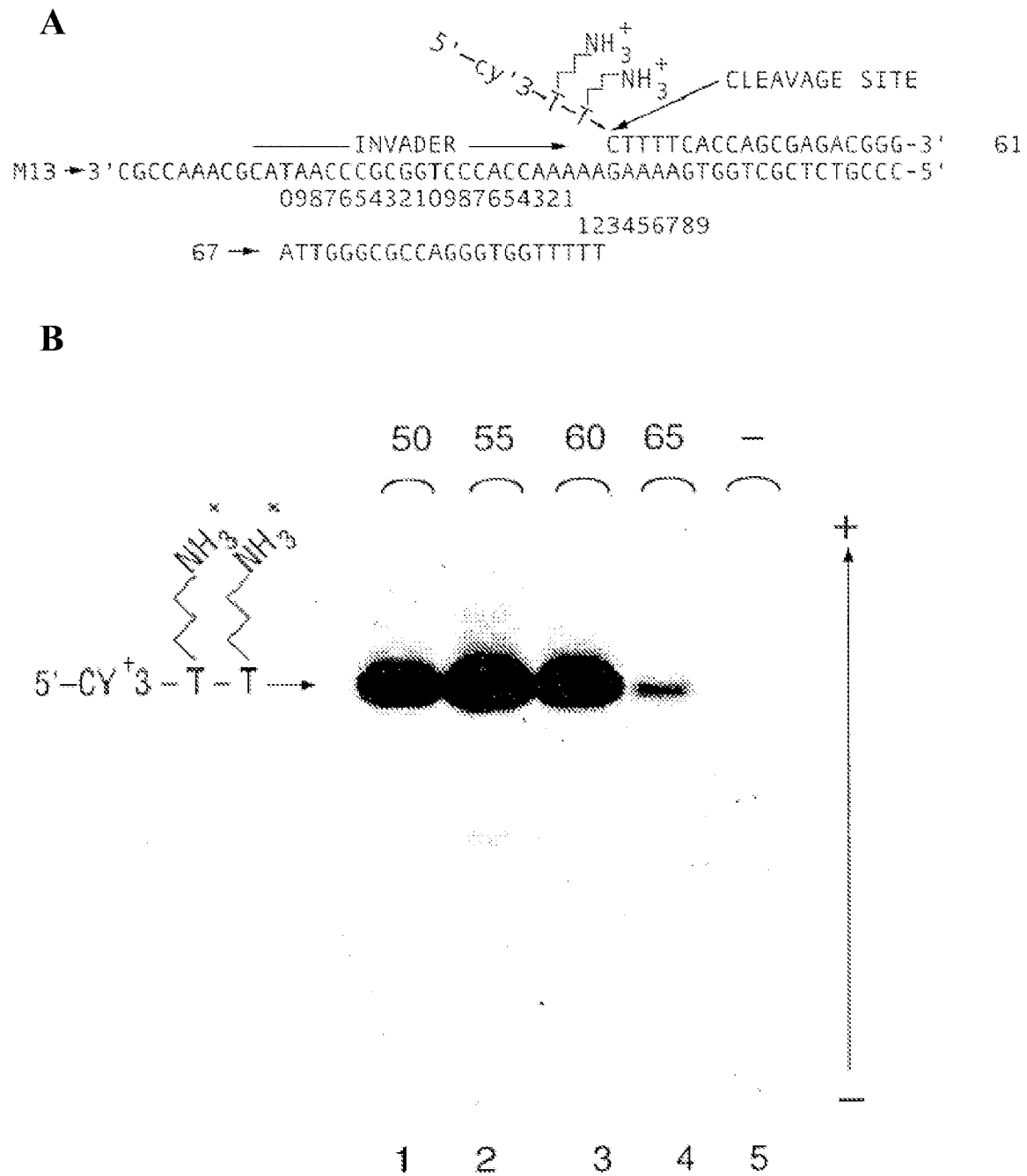


FIGURE 61

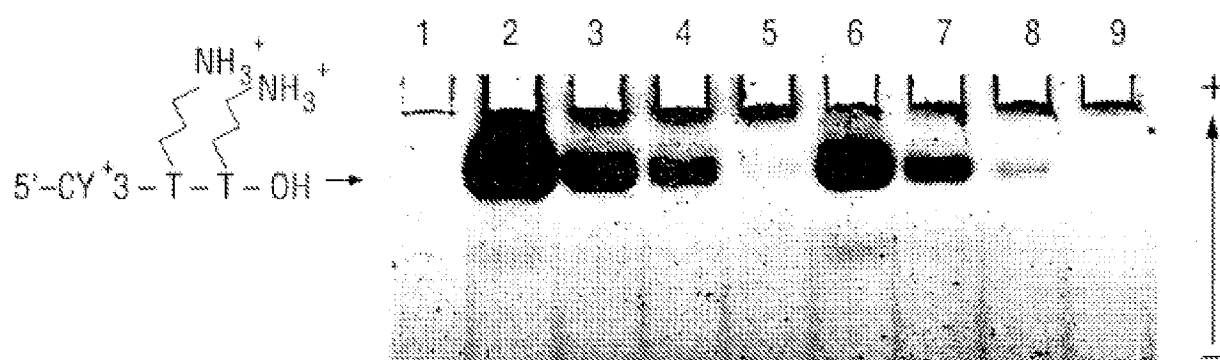


FIGURE 62

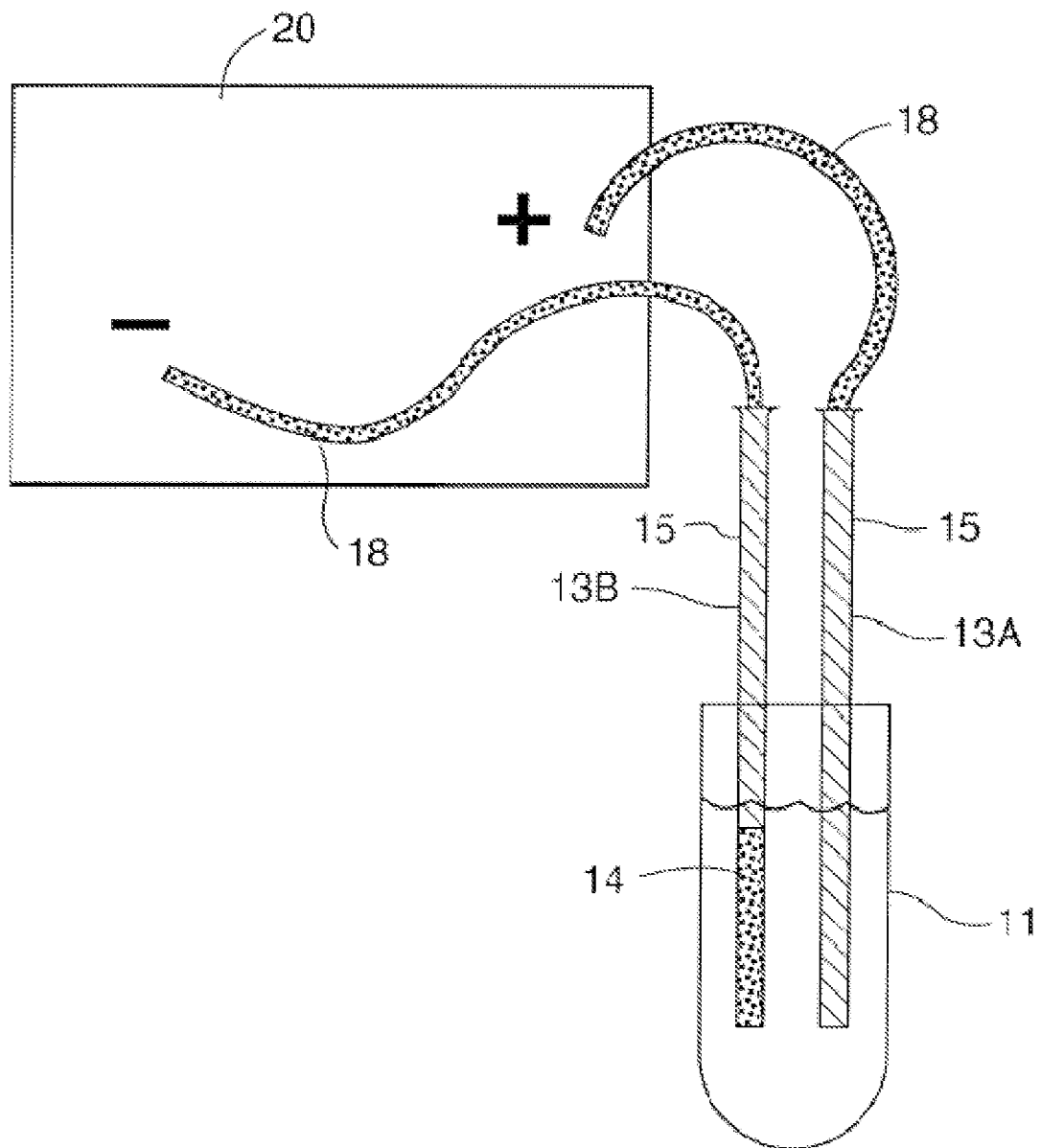


FIGURE 63

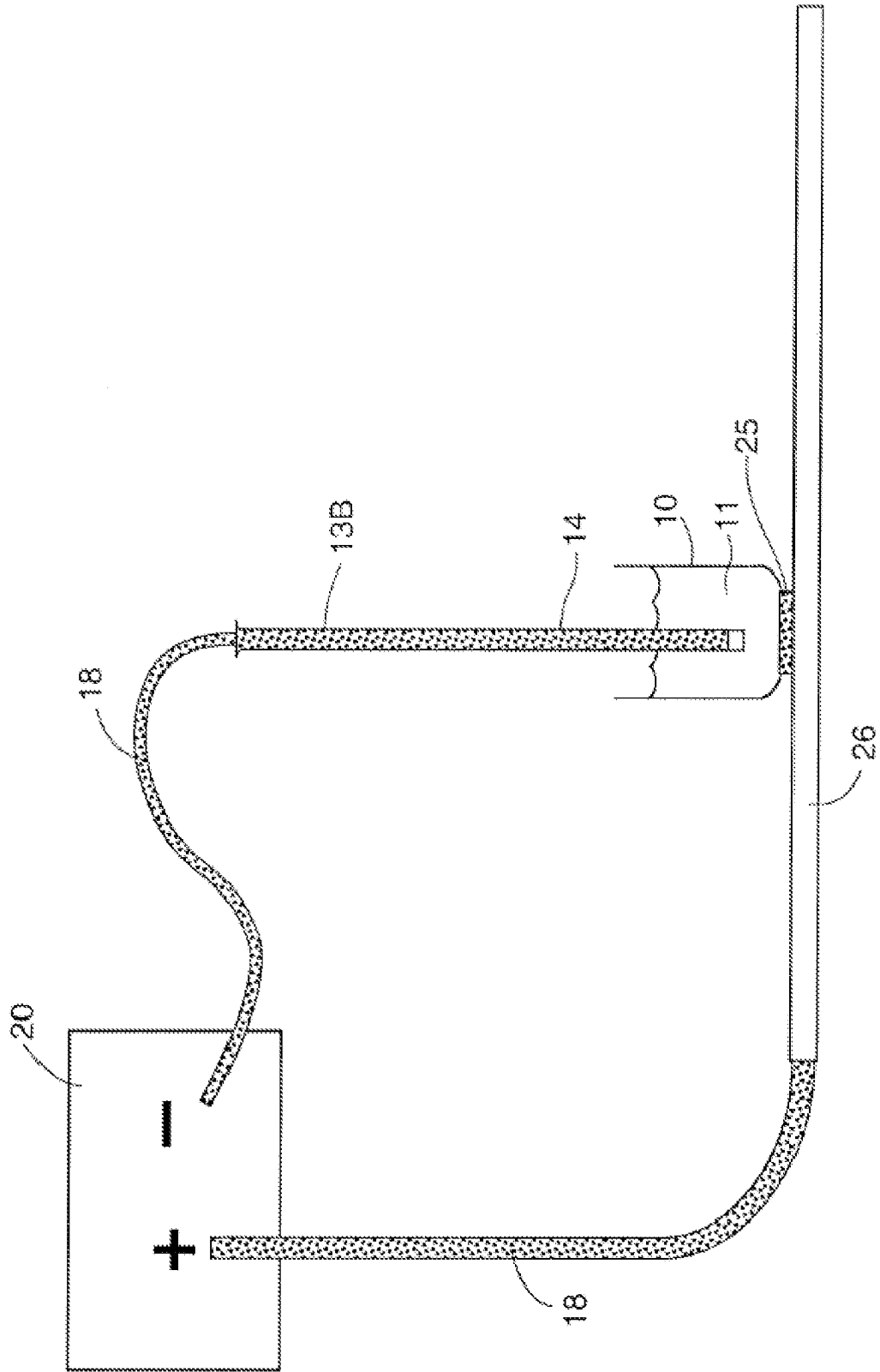


FIGURE 64

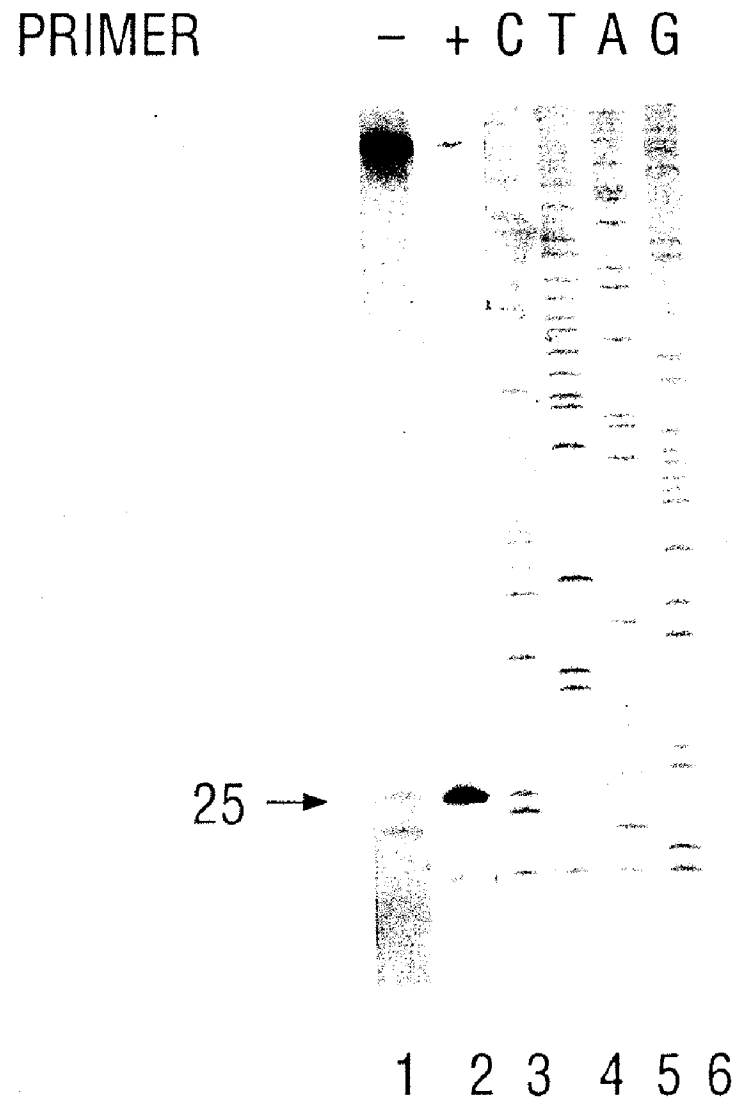
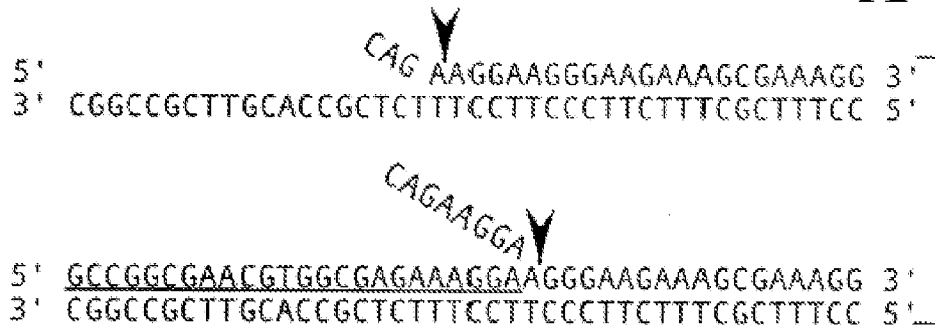
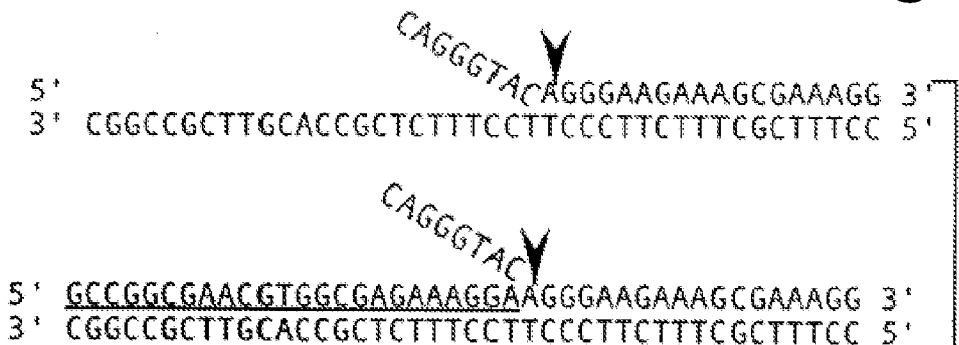


FIGURE 65

**A****B****C****D**

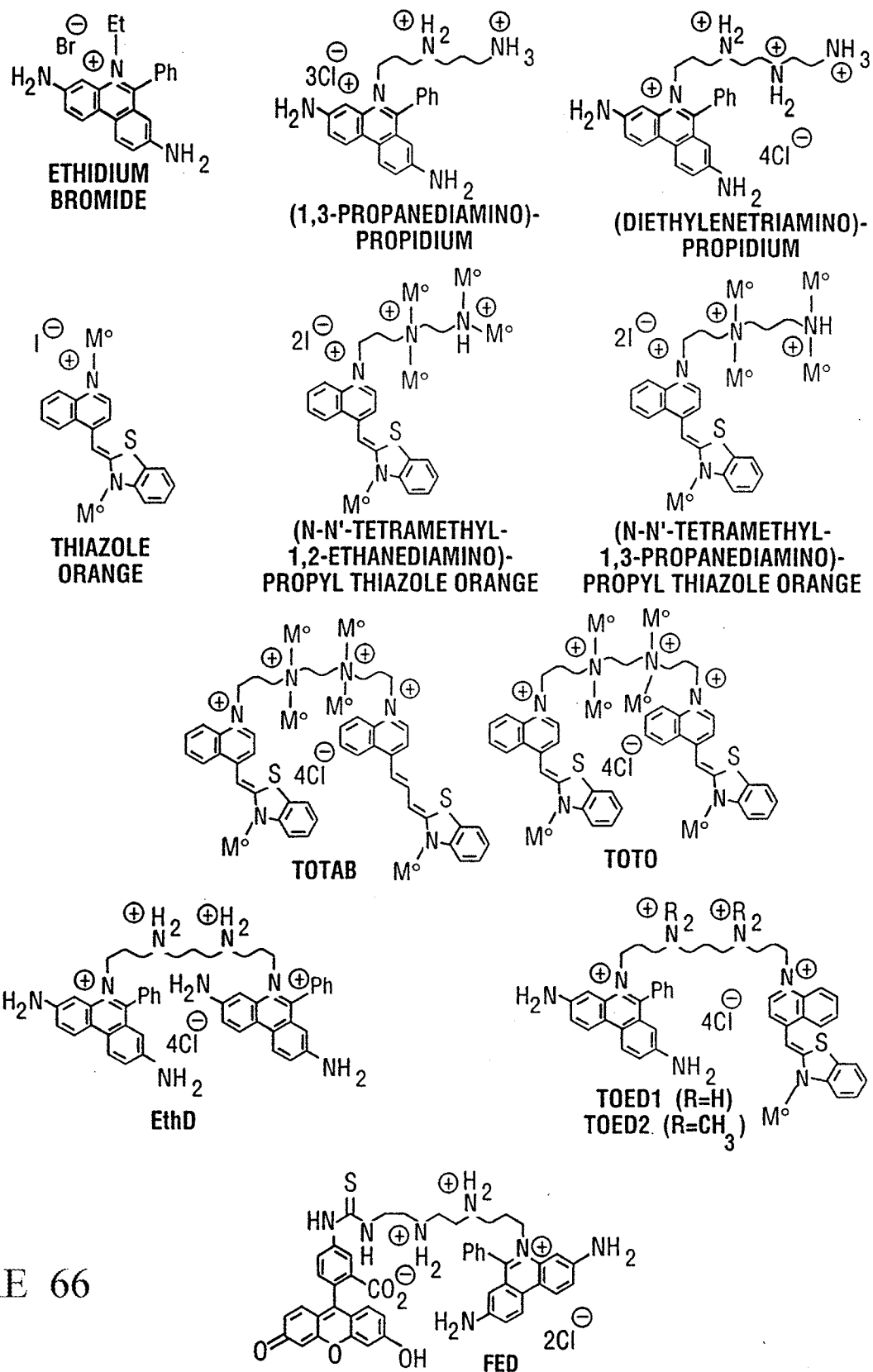


FIGURE 66



FIGURE 67

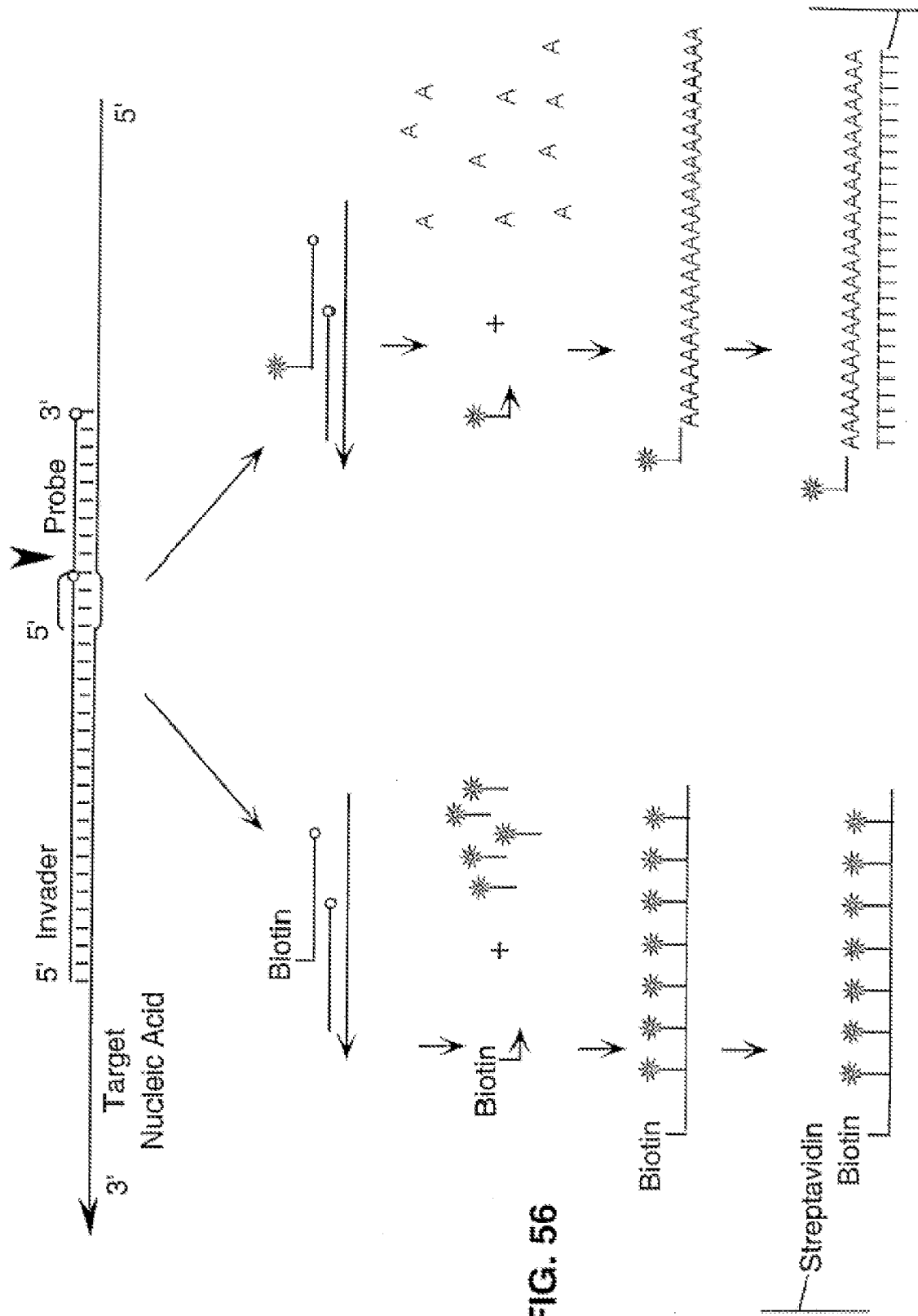
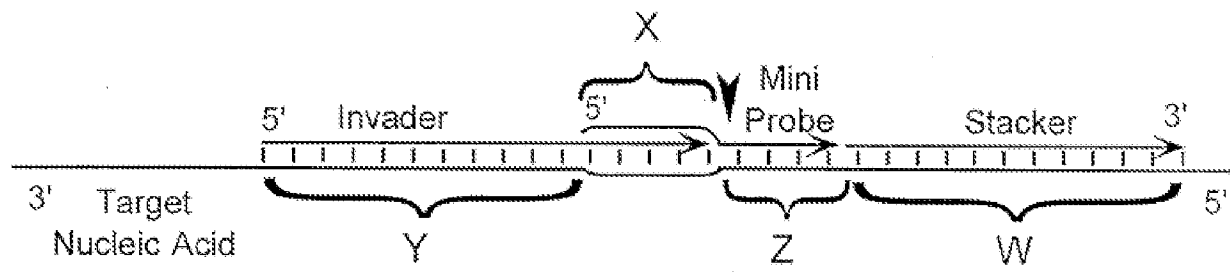


FIG. 56

FIGURE 68



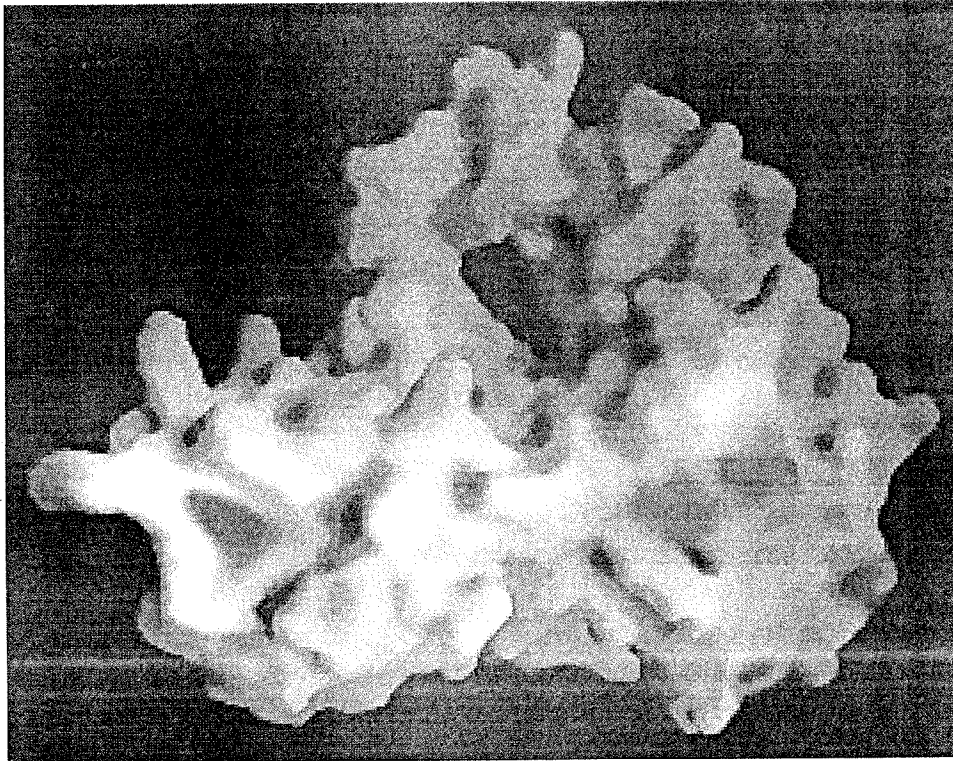


FIGURE 69

FIGURE 70 A

	10	20	30	40	50	60	70									
1	MGVQ----	FGDFIPK--	NIISFEDLKGKKVAIDGMNALYQFLT	SIRLRDGSPLNRKGEITSAYNGVY	MJAFEN1.PRO											
1	MGVP-----	IGEIIIPR--	KEIELENLYGKKIAIDALNAIYQFLST	IRQKDGTPLMDSKGRITSHLSGLFY	PFUFEN1.PRO											
1	MGIQGLAKLI	ADVAPSAI	RENDIKSYFGRKVAIDASMSIYQFLIAVRQ-	GGDVLQNEEGETTSHLMGMFY	HUMFEN1.PRO											
1	MGIHGLAKLI	ADVAPSAI	RENDIKSYFGRKVAIDASMSIYQFLIAVRQ-	GGDVLQNEEGETTSHLMGMFY	MUSFEN1.PRO											
1	MGIKGLNAII	SEHVPSAI	RKSDIKSFFGRKVAIDASMSLYQFLIAVRQDGGQLTNEAGETTSHLMGMFY	YST510.PRO												
1	MGVHSFWDIAG-	-----	PTARPVRLESLEDKRMVADASIWIYQFLKAVRDQEGNAVKN-	-----	SHITGFFR	YSTRAD2.PRO										
1	MGVSGLWNILE-	-----	PVKRPVKLETLVNKRLAIDASIWIYQFLKAVRDKEGNQLKS-	-----	SHVVGFFR	SPORAD13.PRO										
1	MGVQGLWKLE-	-----	CSGROVSPEALEGKILAVDISIWLNQALKGVRDRHGN SIEN-	-----	PHLLTLFH	HUMXPG.PRO										
1	MGVQGLWKLE-	-----	CSGHRVSPALEGKVLAVDISIWLNQALKGVRDSHG NVIEN-	-----	AHLLTLFH	MUSXPG.PRO										
1	MGVQGLWKLE-	-----	CSGRPINPGTLEGKILAVDISIWLNQAVKGARDRQGN AIQN-	-----	AHLLTLFH	XENXPG.PRO										
1	MTINGIWEWA	NHVV----	RKVPNETMRDKTILSIDGHIWLYESLKGCEAHHQQT-	-----	PNSYLVTF	FT CELRAD2.PRO										
	80	90	100	110	120	130	140									
64	KTIHLL	ENDITPI	WVFDGEP	PKLKEK	TRKVRRE	MEKEAEL	KMKEAIKK-----	EDFEEAAKYAKRVSYLTP	MJAFEN1.PRO							
64	RTINL	MEAGIK	PVYVFD	GEPPEF	KKKELE	KRRREAR	EEAEKWR	EAL EK-----	GEIEEARKYAQRATRVNE	PFUFEN1.PRO						
70	RTIRM	MENG	IKPVYV	FDGKPP	QLKSG	ELAKRS	ERRAEAE	KQLQQA	AA-----	GAEOEVEKFTKRLVKVTK	HUMFEN1.PRO					
69	RTIRM-	ENG	IKPVYV	FDGKPP	QLKSG	ELAKRS	ERRAEAE	KQLQQA	EA-----	GMEEEVEKFTKRLVKVTK	MUSFEN1.PRO					
71	RTL	RMIDN	GKPCYV	FDGKPP	DLKSH	ELTKRSS	RRVET	EKKLA--	-EA-----	TTELEKMKQERRLVKVSK	YST510.PRO					
61	RICKLL	YFGI	RPVVF	FDGGV	PVLK	RETIRQ	KERRQ	KGKRES	AKSTARK	LLALQ	LQNGSNDNKRDS	DEV	TM	YSTRAD2.PRO		
61	RICKLL	FFGI	KPVVF	FDGG	APSLK	RQTIQ	KRQARR	LDR	REENAT	VTANK	LLALQMRHQAML	KRDAD	EV	TQ SPORAD13.PRO		
61	RLCKLL	FFRI	RPVF	FDGD	APLLK	KQTLV	KRRQ	KDL	ASSD	SRKTTE	KLKTFL	KRQAIK	TERIA	AT	VTG HUMXPG.PRO	
61	RLCKLL	FFRI	RPVF	FDGD	APLLK	KQTLV	KRRQ	KDL	ASSD	SRKTTE	KLKTFL	KRQAL	KTDRIA	AS	VTG MUSXPG.PRO	
61	RLCKLL	FFRI	RPVF	FDGE	APLLK	RQTLA	KRRQR	TOKAS	NDARK	TNEKL	RTFL	KRQAIK	AERIA	AT	VTG XENXPG.PRO	
60	RIORL	LEKII	PIVVF	DNIN	ASSA	HESK	DQNEF	VPKR	RRSFG	DS	PFTNI	V-----	-----	-----	-----	CELRAD2.PRO

FIGURE 70 B

	150	160	170	180	190	200	210
130	KMVENCKYLLSLMGIPYVEAPSEGEAQASYMAKKGDVWVVSQDYDALLYGAPRVVRNLTTTKEM----						MJAFEN1.PRO
130	MLIEDAKKLLLELMGIPYVQAPSEGEAQAAAYMAAKGSVYASASQDYDLSLLFGAPRLVRNLTTITGKRKLPGK						PFUFEN1.PRO
136	QHNDCKHLLSLMGIPYLDAPSEAEASCAALVKAGKVYAAATEDMDCLTFGSPVLMRHLTASEAKKLPQ						HUMFEN1.PRO
134	QHNDCKHLLSLMGIPYLDAPSEAEASCAALAKAGKVYAAATEDMDCLTFGSPVLMRHLTASEAKKLPQ						MUSFEN1.PRO
134	EHNEEAQKLLGLMGIPYIIAPTAEAAQCAELAKKGVYAAASEDMOTLCYRTPFLLRHLTFSEAKKEPIH						YST510.PRO
131	OMIKEVQELLSRFGIPYITAPMEAEQAELQLNLVDGIIITDSDSVFLFGGTYKVMFHEKNY----						YSTRAD2.PRO
131	VMIKECQELLRLFGIPYIVAPOEAEQAQCSKLELKLVDGIVTDSDSVFLFGGTRVYRNMFNQKFN----						SPORAD13.PRO
131	QMFLESQELLRLFGIPYIQAPMEAEQAQCAILDLTQDTSGTITDSDIWLFGARHVYRNFNKNKF----						HUMXPG.PRO
131	QMFLESQELLRLFGVPIYIQAPMEAEQAQCAVLDSLQDTSGTITDSDIWLFGARHVYKFNKNKF----						MUSXPG.PRO
131	QMCLESQELLQLFGIPYIVAPMEAEQAQCAILDLTQDTSGTITDSDIWLFGARHVYKNFFSQNKH----						XENXPG.PRO
111	OHVYKTNALLTELGIKVIIIAPGGEAQCARLEQLQGVTSGCITTDYFDYFLFGKNLYRDEFTAGT-----						CELRAD2.PRO
	220	230	240	250	260	270	280
195	-----PELIELNEVLEDLRISLQDLIDIAIFMGTDYNPGGV--K--GIGFKRAYELVRSGVAK--DV						MJAFEN1.PRO
200	NVYVE-IKPELIIIEEVKELKLTREKLIELAILVGTDYNPGGI--K--GIGLKKALEIVRHSKDPLAKF						PFUFEN1.PRO
206	EFHLSRILQELGLNQEQFVDLCILLGSDYCESIRGIGPKRAVDLIQK--HKSIEEIVRRLDPN----						KYHUMFEN1.PRO
204	EFHLSRVLQELGLNQEQFVDLCILLGSDYCESIRGIGAKRAVDLIQK--HKSIEEIVRRLDPS----						KYMUSFEN1.PRO
204	EIDTELVLRLGLDLTIEQFVDLCIMLGCDYCESIRGVGPVTALKLIKT--HGSIEKIVEFIESGESNNTKW						YST510.PRO
198	FYDAESI KLLGLDRKNMIELAQLLGSDYTNGLKMGMPVSSIEVIAEF--GNLKNFKDWNNGOFDKRK						YSTRAD2.PRO
198	LYLMDDMKREFNVNQMDLIKLAHLGSDYTMGLSRVGPVLALEILHEFFPGDTGLFEKKWFQRLSTGHAS						SPORAD13.PRO
198	YYQYVDFHNLGLDRNKLINLAYLLGSDYTEGIPTVGCVTAMEILNEFFPGHGLEPLLKFSEWWHEAQKNP						HUMXPG.PRO
119	YYQYVDFYSQGLDRNKLINLAYLLGSDYTEGIPTVGCVTAMEILNEFFPGRLDPLLLKFSEWWHEAQNNK						MUSXPG.PRO
198	YYQYADIHNOLGLDRSKLINLAYLLGSDYTEGIPTVGVYSAMEILNEFFPGQGLEPLVKFKEMWSEAKQDK						XENXPG.PRO
175	-----SSTACLHIDIMHLSLGRMF-----						CELRAD2.PRO

FIGURE 70 C

	290	300	310	320	330	340	350
251	LKKEVEYYDEIKRIFKEPKV	-----	-----	-----	-----	-----	MJAFEN1.PRO
265	QKQSDVDLYAIKEFFLNPPV	-----	-----	-----	-----	-----	PFUFEN1.PRO
269	PVPENWLHKEAHQLFLEPEV	-----	-----	-----	-----	-----	HUMFEN1.PRO
267	PVPENWLHKEAQQLFLEPEV	-----	-----	-----	-----	-----	MUSFEN1.PRO
272	KIPEDWPYKQARMFLDPEV	-----	-----	-----	-----	-----	YST510.PRO
265	QETENKFEKDLRKKLVNNEI	ILDDDFPSVMVYDAYMRPEV	-----	-----	-----	-----	YSTRAD2.PRO
268	KNDVNTPVKKRINKLVGK	-IILPSEFPNPLVDEAYLHPAVDD	SKQSFWQGI	PDLDLDEL	RQFLMATV	GWSKQ	SPORAD13.PRO
268	KIRPNPHDTKVKKKL	--RTLQLTPGFPNPAVAEAYLKP	VVDOSKGSFLW	GKPDLDK	IREFCORY	FGWNRT	HUMXPG.PRO
268	KVAENPYDTKVKKKL	--RKLQLTPGFPNPAVADAYLR	PVVDSDSGSFLW	GKPDVDK	IREFCORY	FGWNRM	MUSXPG.PRO
268	KMRPNPNDTKVKKKL	--RLLDLQQSFPNPAVASAYLKP	VVDDESKSAFSWGR	PDLEQIRE	FCESRFGW	YRL	XENXPG.PRO
194	-----EKKVSRPHLISTAIL	LGCDYFORGVQNI	GIVSVFD	-ILGEFCODG	NEEDPHVIL	DRFASYVRE	CELRAD2.PRO
	360	370	380	390	400	410	420
300	RVKKHVDKLYNLIA	-----	-----	-----	-----	-----	MJAFEN1.PRO
314	RVKNGLERLKKAI	-----	-----	-----	-----	-----	PFUFEN1.PRO
320	RIRSGVKRLSKSRQGS	-TQGR	LDFFKVT	-----	-----	-----	HUMFEN1.PRO
318	RIRSGVKRLSKSRQGS	-TQGR	LDFFKVT	-----	-----	-----	MUSFEN1.PRO
323	RVKSGISRLKGLKSG	-IQGR	LDGFFOVV	-----	-----	-----	YST510.PRO
335	KSDEILPLIRDVNKRKK	-----	-----	-----	-----	-----	YSTRAD2.PRO
337	RTNEVLLPVIQDMHKKOF	-----	-----	-----	-----	-----	SPORAD13.PRO
336	KTDESILFPVLKQLDAQQT	QLRIDSF	FLAQKEKEDAKRIKS	QRLNRAVTC	MLRKEKEA	AASEIEAVSVAM	HUMXPG.PRO
336	KTDESILYPVLKHLNAHQ	TLRIDSF	FLAQKEKQDAKLIK	SHRLSRAVTC	MLRKEEKE	KAPELTKVTEAM	MUSXPG.PRO
336	KTDEVLLPVLKQLNAQQT	QLRIDSF	FLAQKEHEAAG	--LKSQRL	RRAVTC	MKRKERDVEA	EVEAAVAM
257	EIPARSED	TQKRLRLRRKKYNF	PVGFPNCD	AVHNAITMYL	RPPVSSEIPK	IIPR	-----AANFQQVAEIM

314	-----	430	440	450	460	470	480	490	MJAFEN1.PRO
327	-----	-----	-----	-----	-----	-----	-----	-----	PFUFEN1.PRO
348	-----	-----	-----	-----	-----	-----	-----	-----	HUMFEN1.PRO
346	-----	-----	-----	-----	-----	-----	-----	-----	MUSFEN1.PRO
351	-----	-----	-----	-----	-----	-----	-----	-----	YST510.PRO
357	-----	-----	-----	-----	-----	-----	-----	-----	YSTRAD2.PRO
359	-----	-----	-----	-----	-----	-----	-----	-----	SPORAD13.PRO
406	-----	-----	-----	-----	-----	-----	-----	-----	HUMXPG.PRO
406	-----	-----	-----	-----	-----	-----	-----	-----	MUSXPG.PRO
403	-----	-----	-----	-----	-----	-----	-----	-----	XENXPG.PRO
322	-----	-----	-----	-----	-----	-----	-----	-----	CELRAD2.PRO
314	-----	-----	-----	-----	-----	-----	-----	-----	NKTQKTL MJAFEN1.PRO
327	-----	-----	-----	-----	-----	-----	-----	-----	KSGKQSTL PFUFEN1.PRO
352	-----	-----	-----	-----	-----	-----	-----	-----	KKAKTGAAG HUMFEN1.PRO
350	-----	-----	-----	-----	-----	-----	-----	-----	KKAKTGGAG MUSFEN1.PRO
354	-----	-----	-----	-----	-----	-----	-----	-----	NKKLNKNKNK YST510.PRO
364	-----	-----	-----	-----	-----	-----	-----	-----	PREYISGDKKLNTSKRISTATGKL YSTRAD2.PRO
429	-----	-----	-----	-----	-----	-----	-----	-----	RRKMMASKNSSDSDSEDNFLASLTPKTNSSSISIENLPRKTKLSTSL SPORAD13.PRO
476	-----	-----	-----	-----	-----	-----	-----	-----	NVQRRTAAKEPKTSASDSOHSVKEAPVKNKGATTSSSDSDDBDGKKEKMLVLTARSVFGKKRRKLRRARG HUMXPG.PRO
469	-----	-----	-----	-----	-----	-----	-----	-----	SARQRSAAESSKIGCDVPLVRDSPHGRQGCVSTSSDSEDGEDKAKTVLVTARPVFGKKRRKLKSMK MUSXPG.PRO
458	-----	-----	-----	-----	-----	-----	-----	-----	WNRKRKRSESPQILQHHAKRQVPDRK GSSSDAEDLPSGLIDKQSQSGIVGROKASNKVSSSSDDEDRVTMVTAKEPVFQKKTKSKTMKE XENXPG.PRO
387	-----	-----	-----	-----	-----	-----	-----	-----	WNRKRKRSESPQILQHHAKRQVPDRK RSVKIRAFKPYPTDVI CELRAD2.PRO

## FIGURE 70 E

322 DAWFKZ  
335 ESWFKR  
375 KFKRGK  
373 KFRRGK  
377 VTKGRR  
390 --RKM  
483 SKRRRK  
546 RKRKTZ  
538 RRKKKT  
523 TVKRK  
429 ELGDSO

MJAFEN1.PRO  
PFUFEN1.PRO  
HUMFEN1.PRO  
MUSFEN1.PRO  
YST510.PRO  
YSTRAD2.PRO  
SPORAD13.PRO  
HUMXPG.PRO  
MUSXPG.PRO  
XENXPG.PRO  
CELRAD2.PRO



FIGURE 71



FIGURE 72

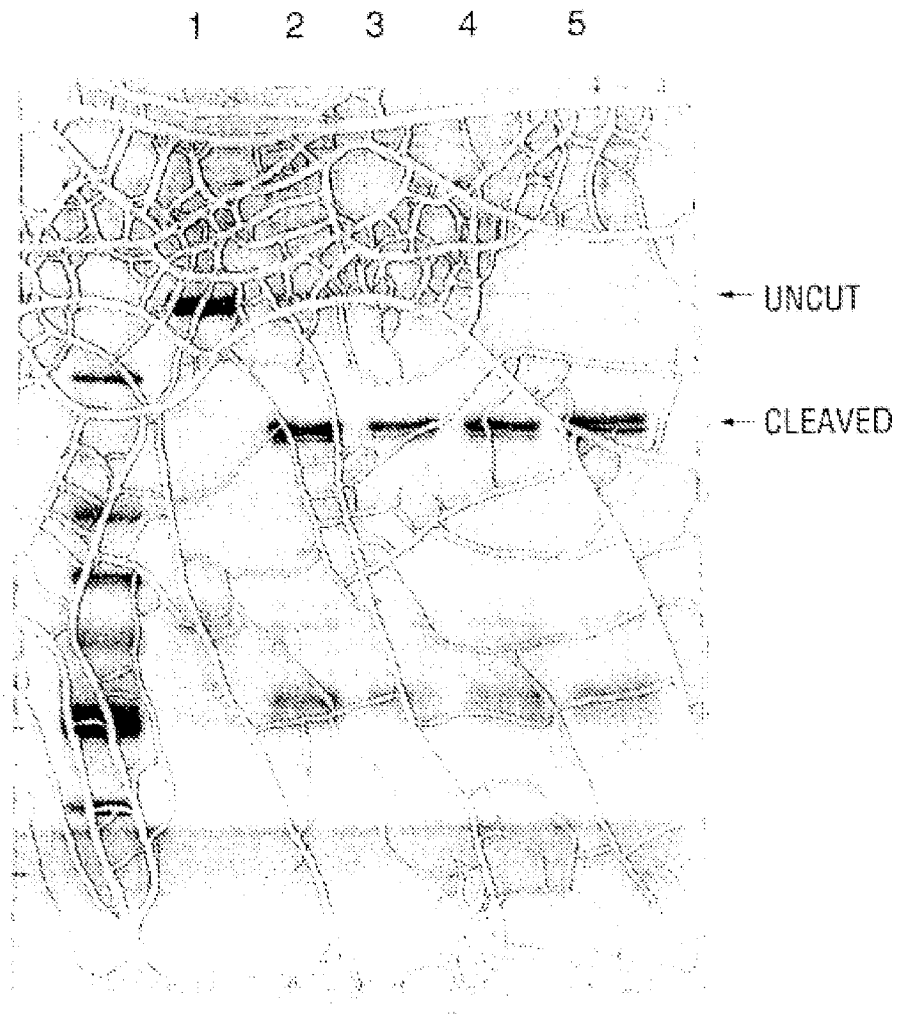


FIGURE 73

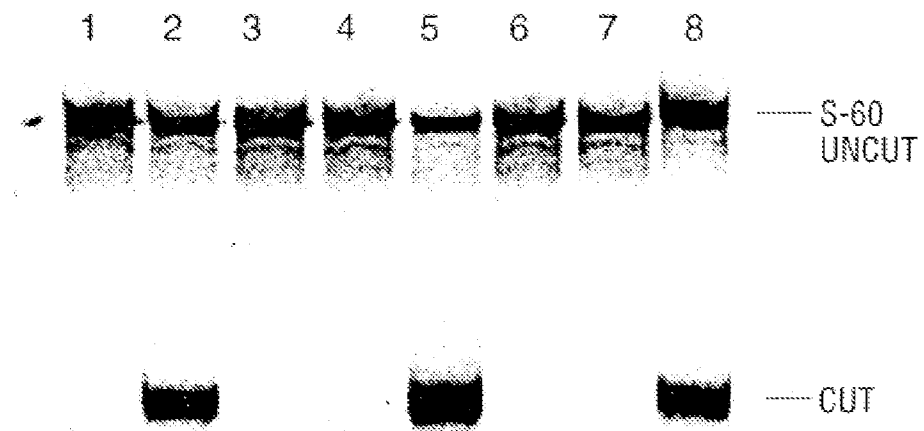


FIGURE 74

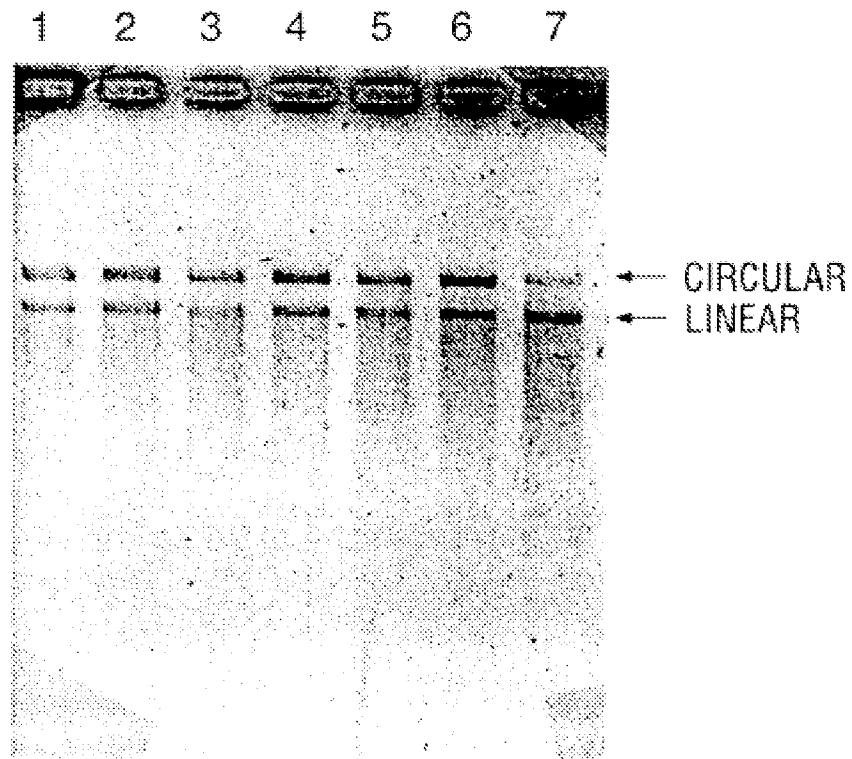


FIGURE 75

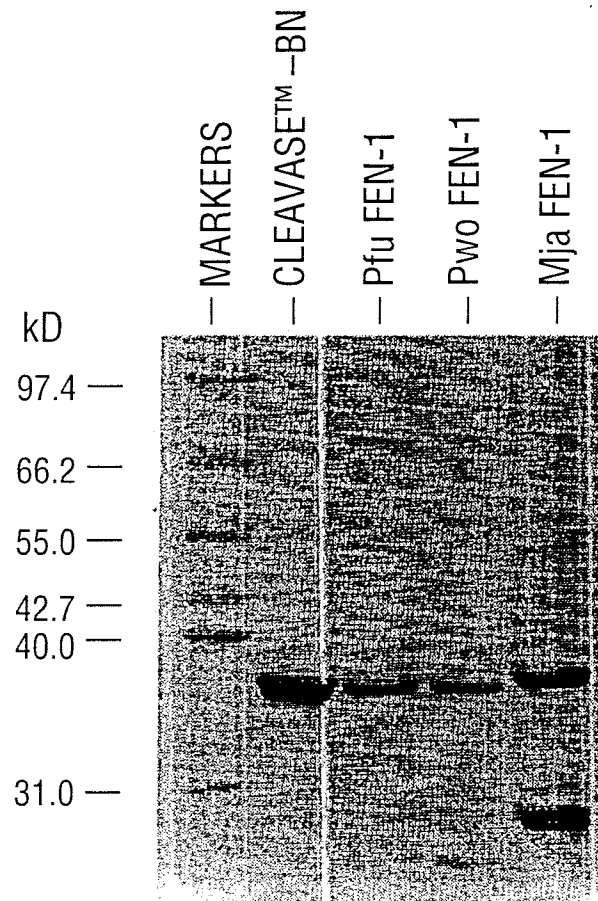


FIGURE 76

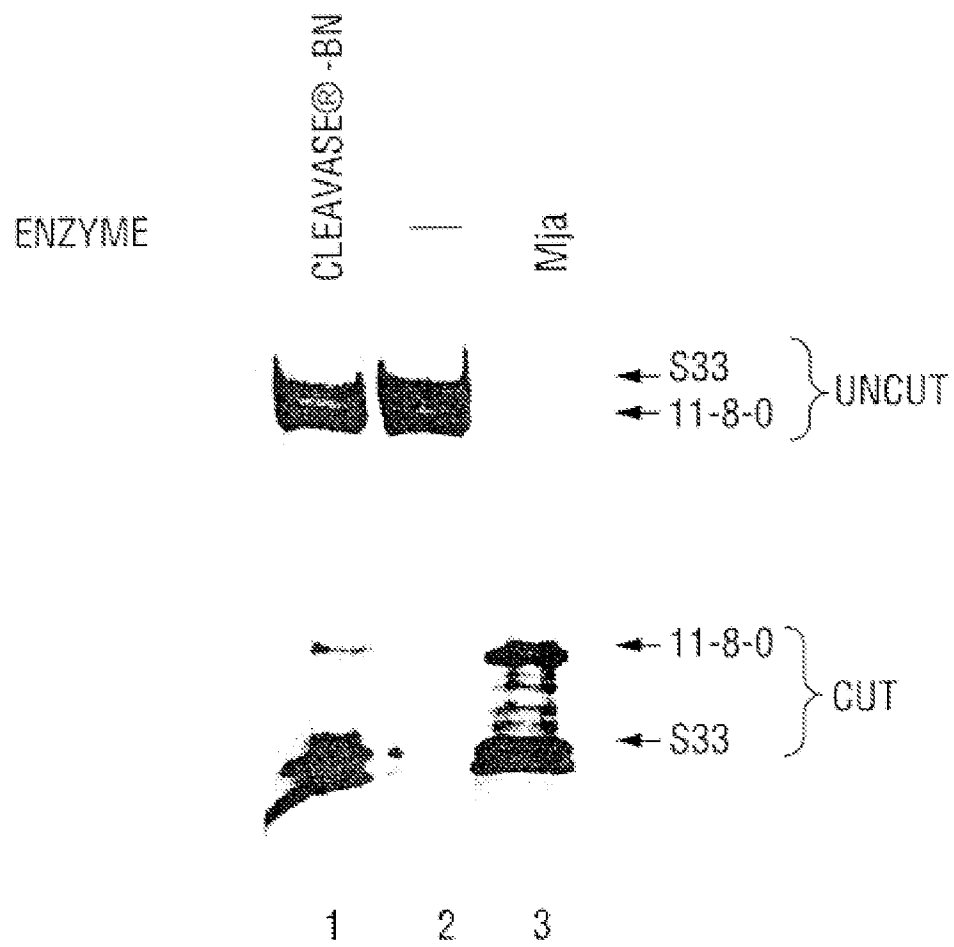


FIGURE 77

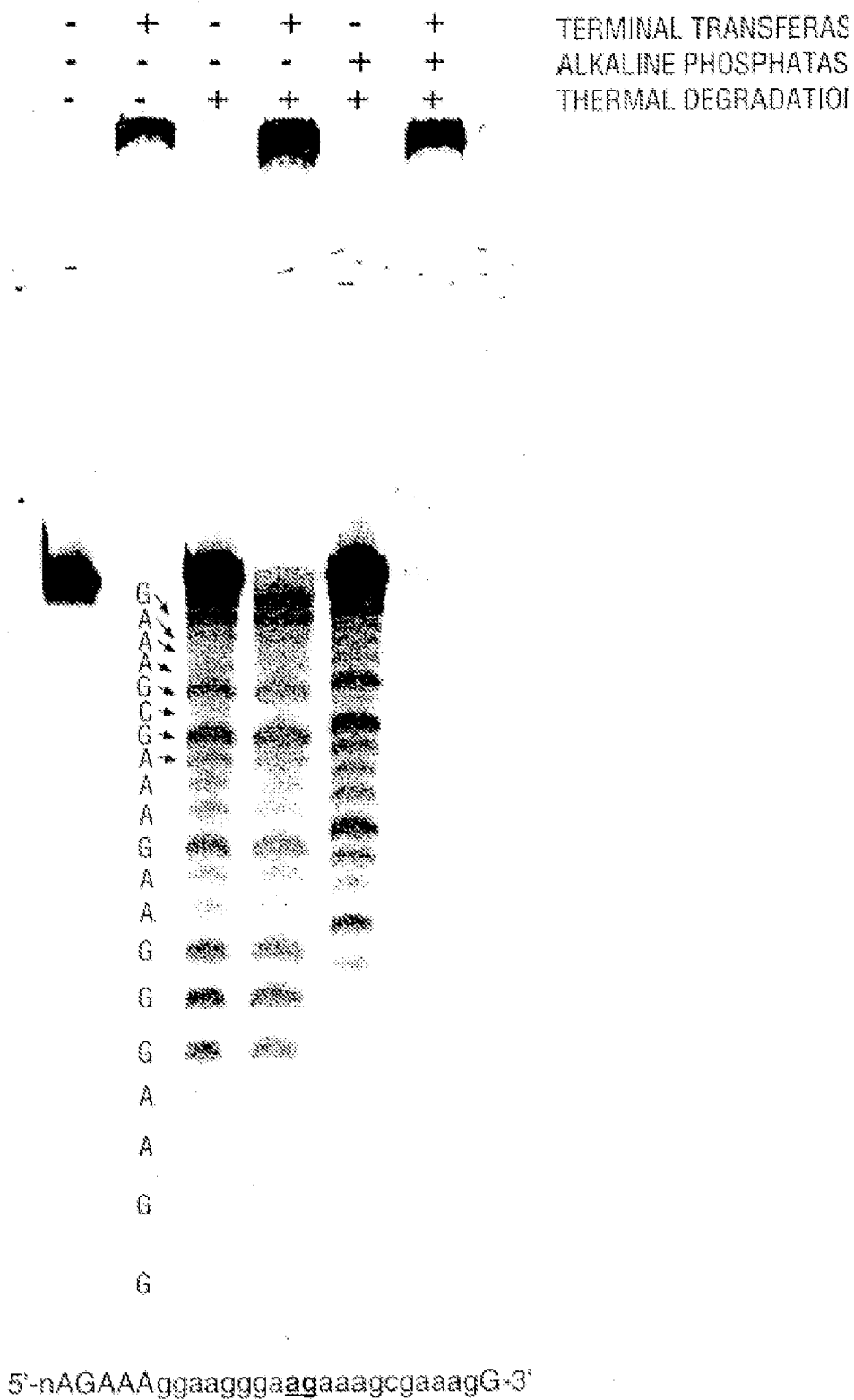
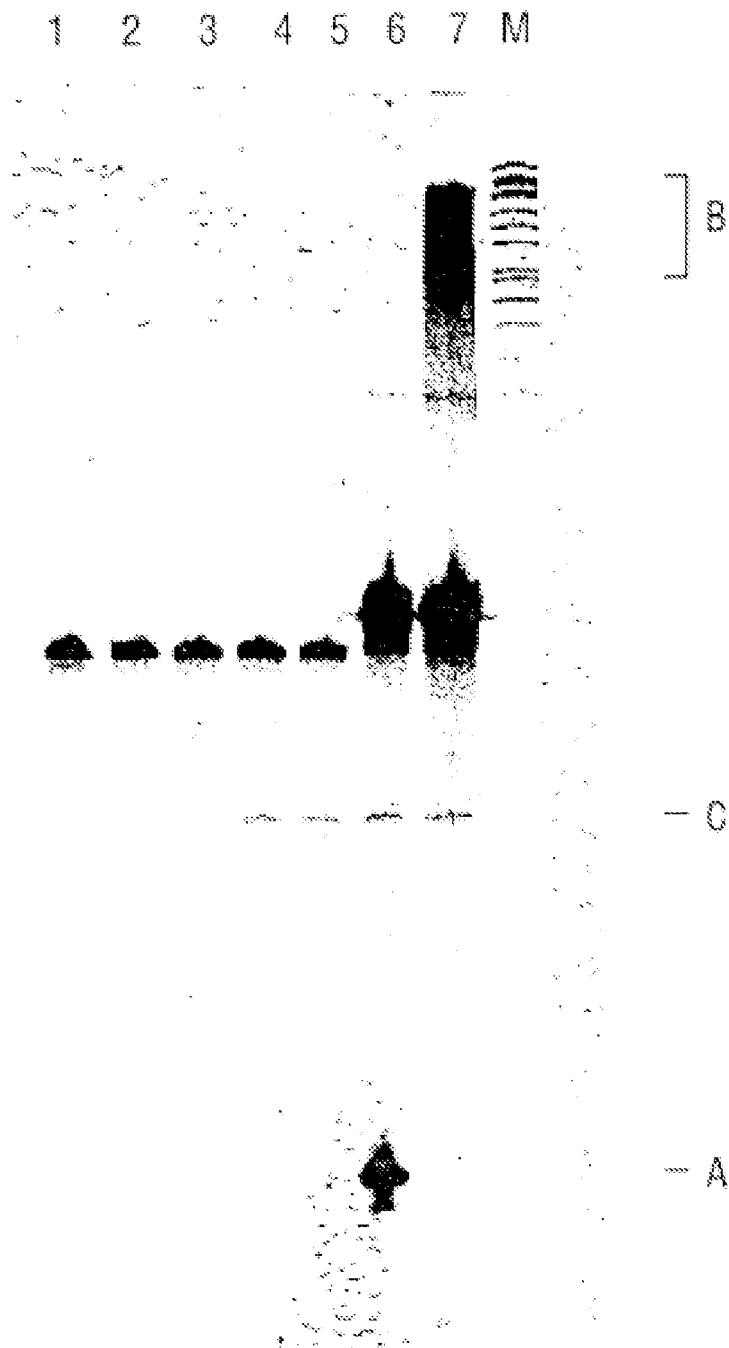


FIGURE 78





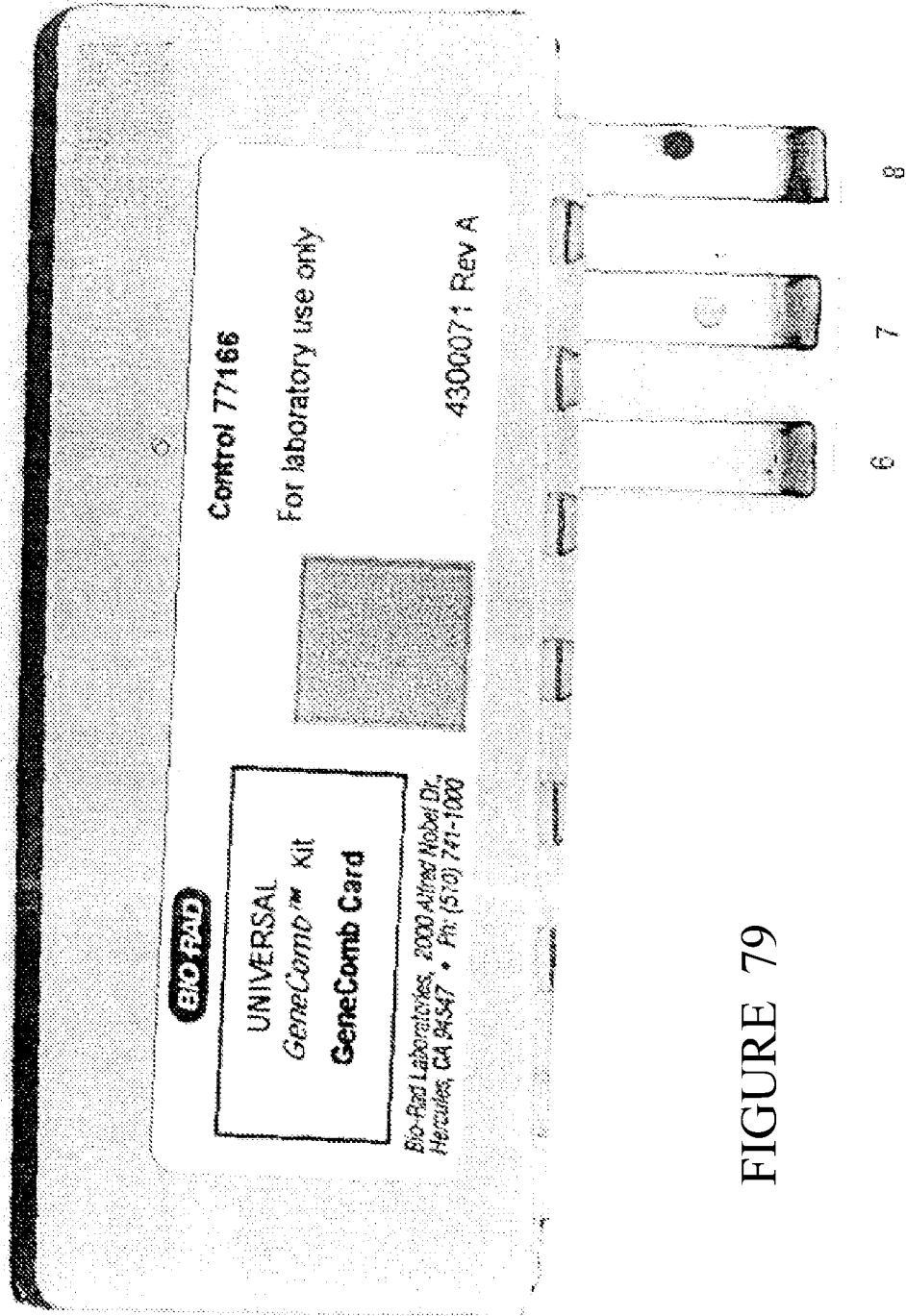


FIGURE 79

FIGURE 80

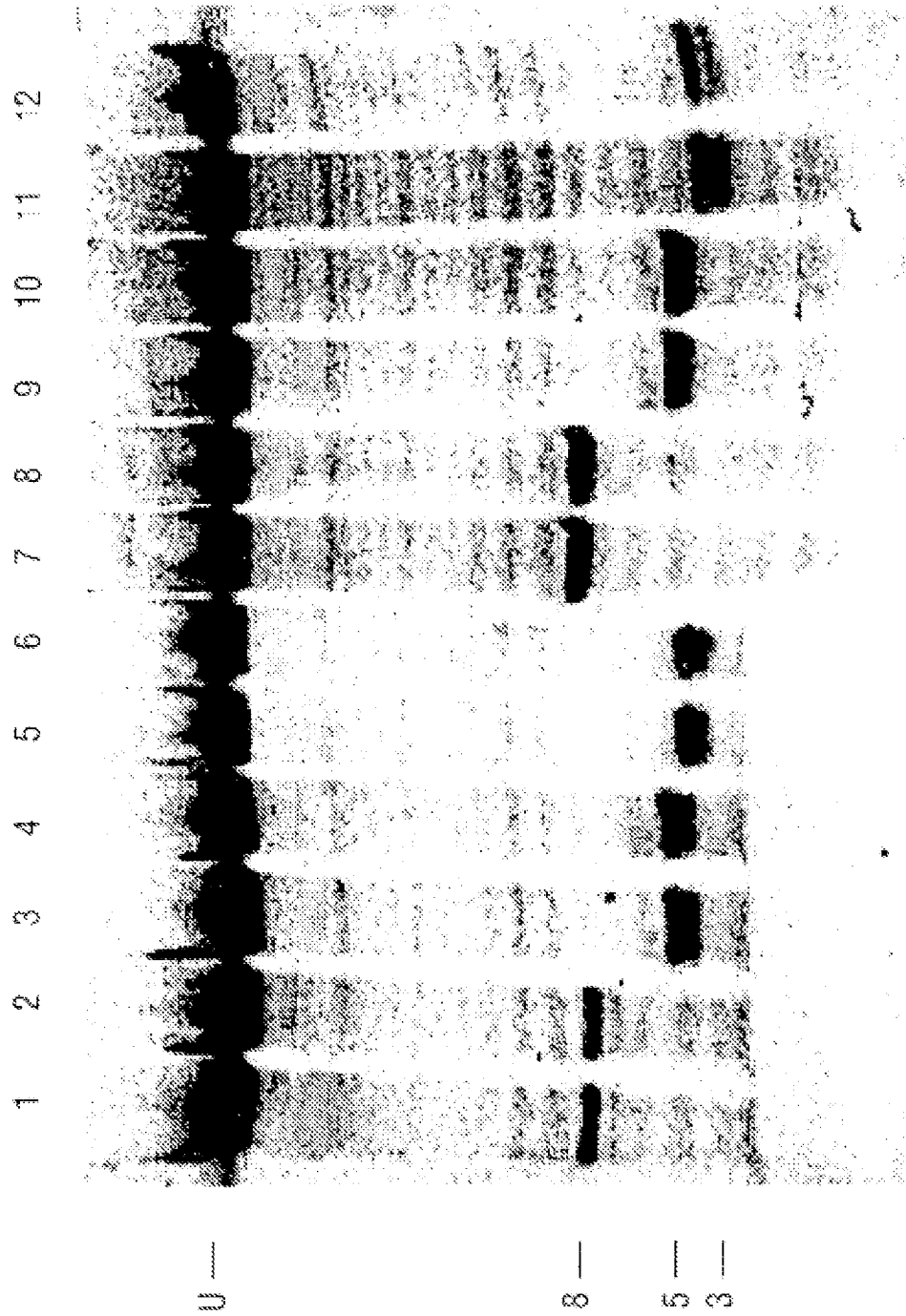


FIGURE 81

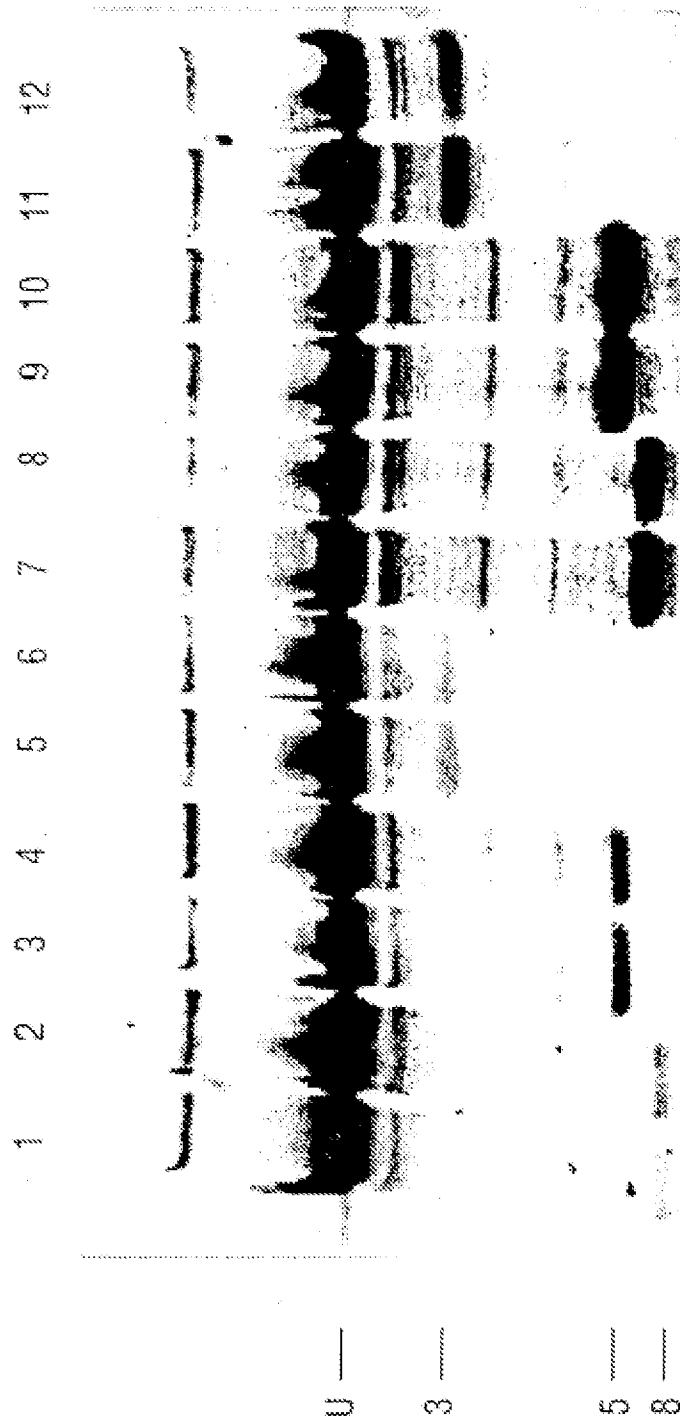


FIGURE 82

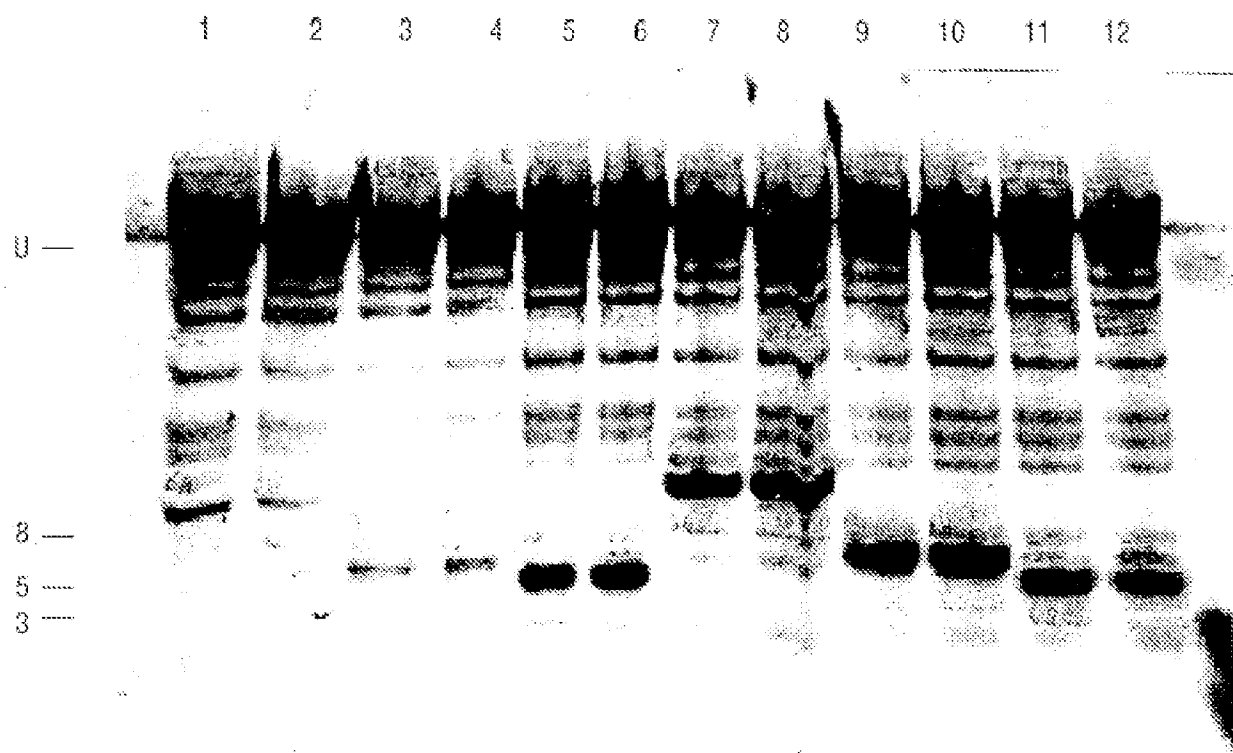


FIGURE 83

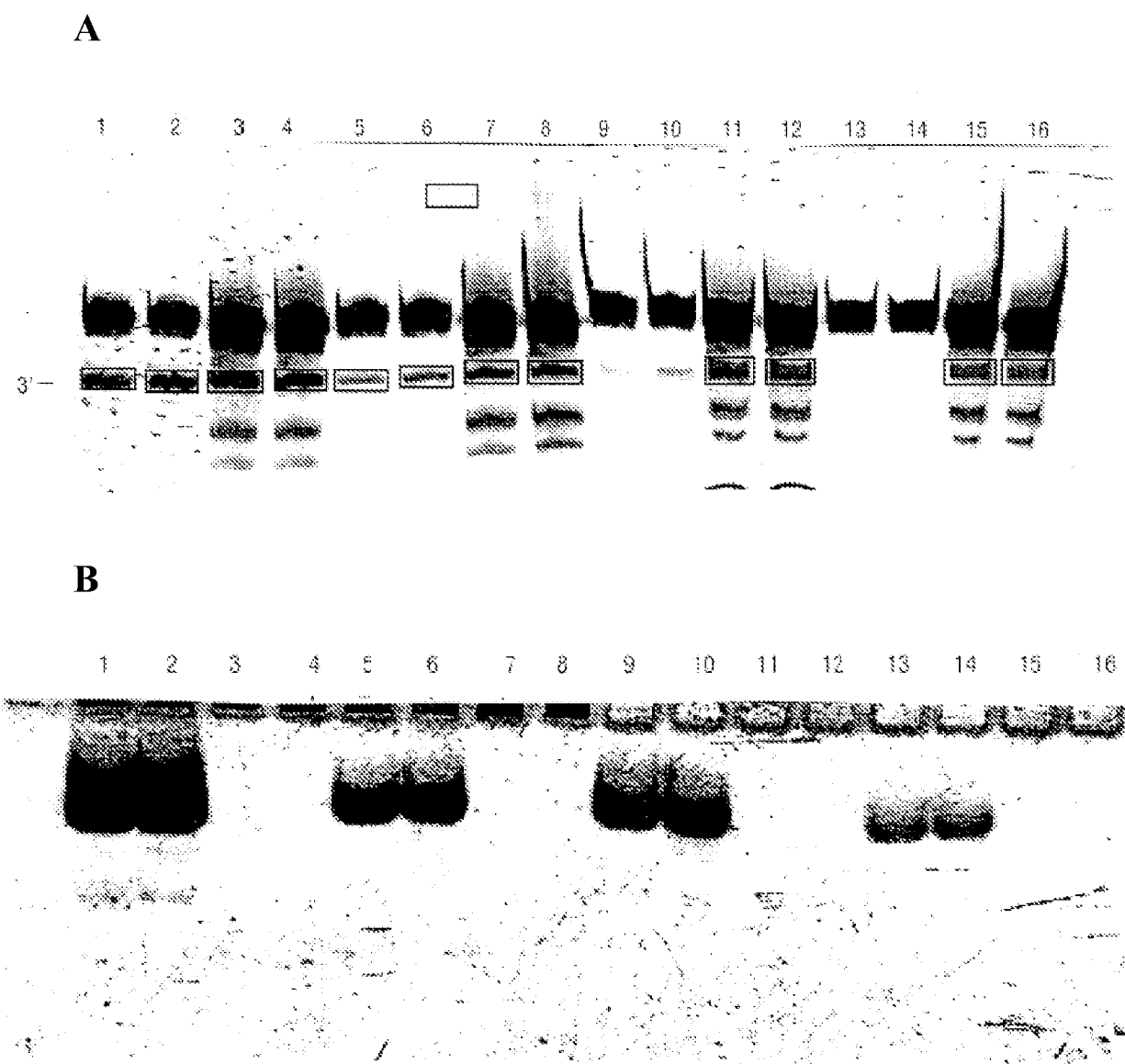


FIGURE 84

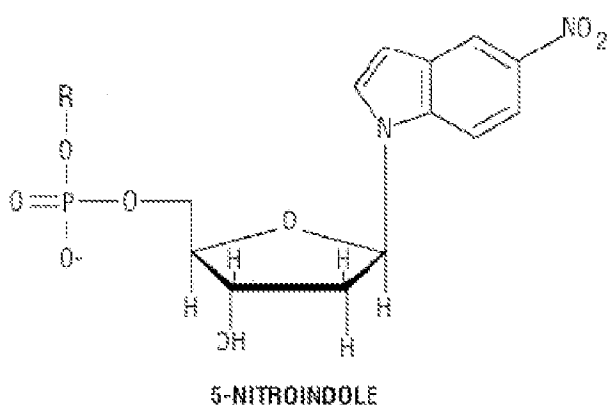
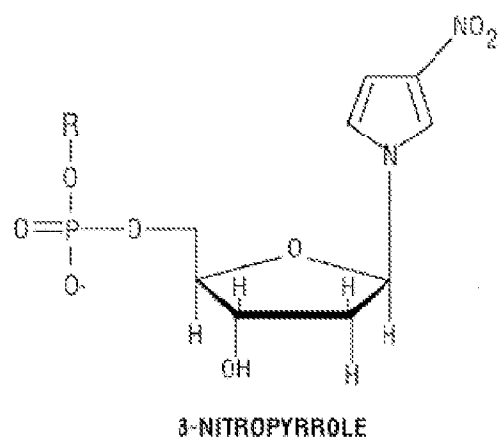


FIGURE 85

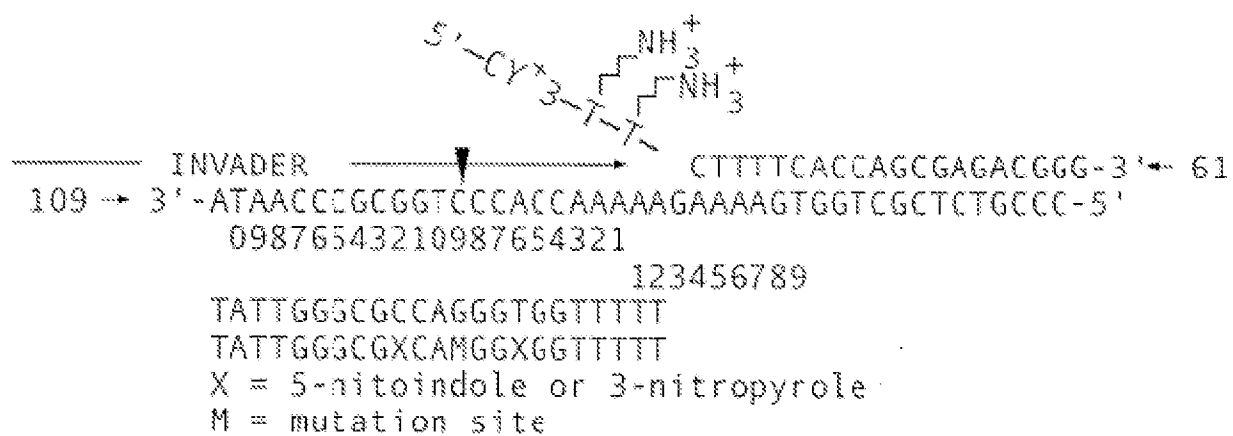


FIGURE 86

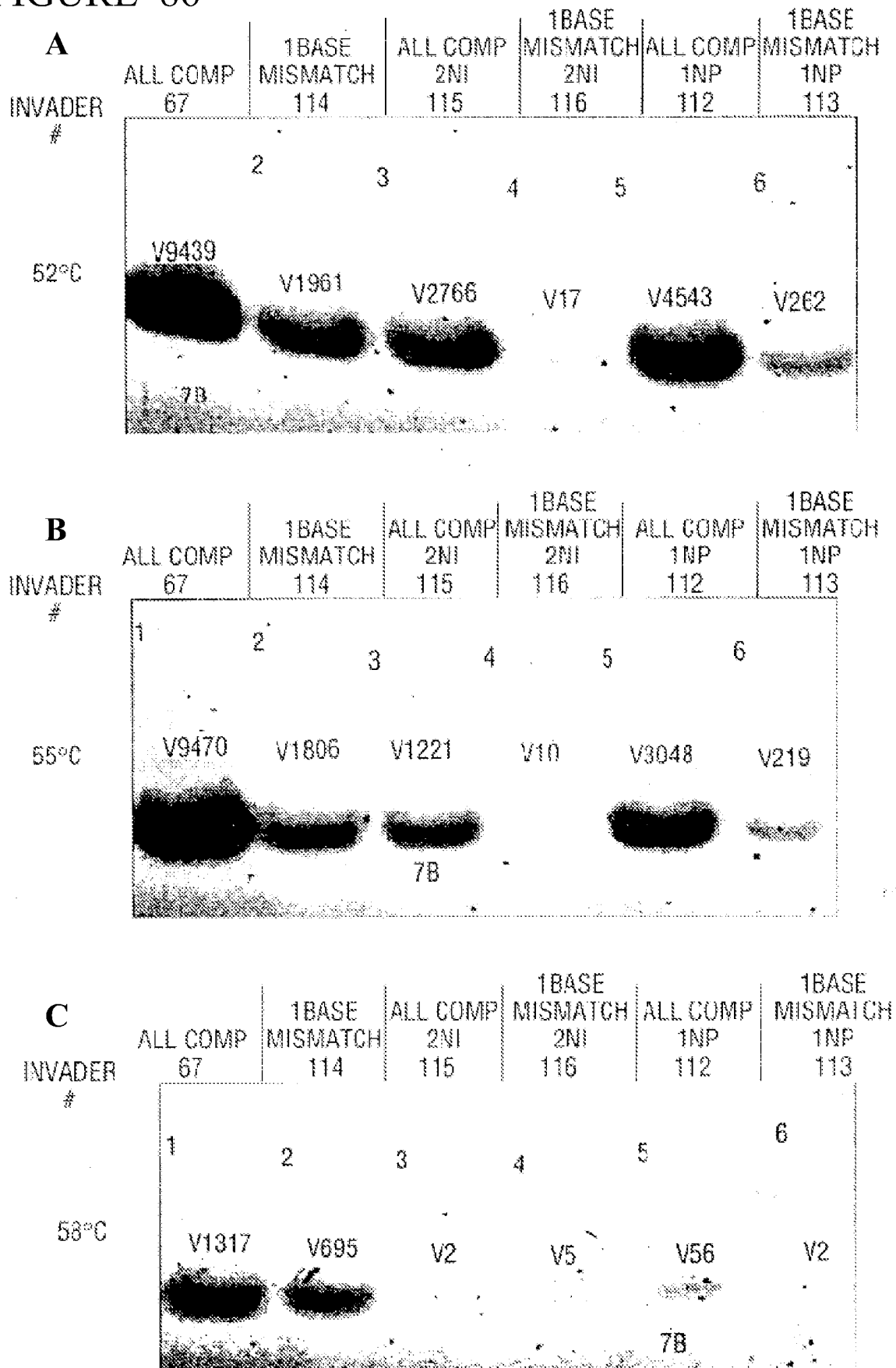




FIGURE 87

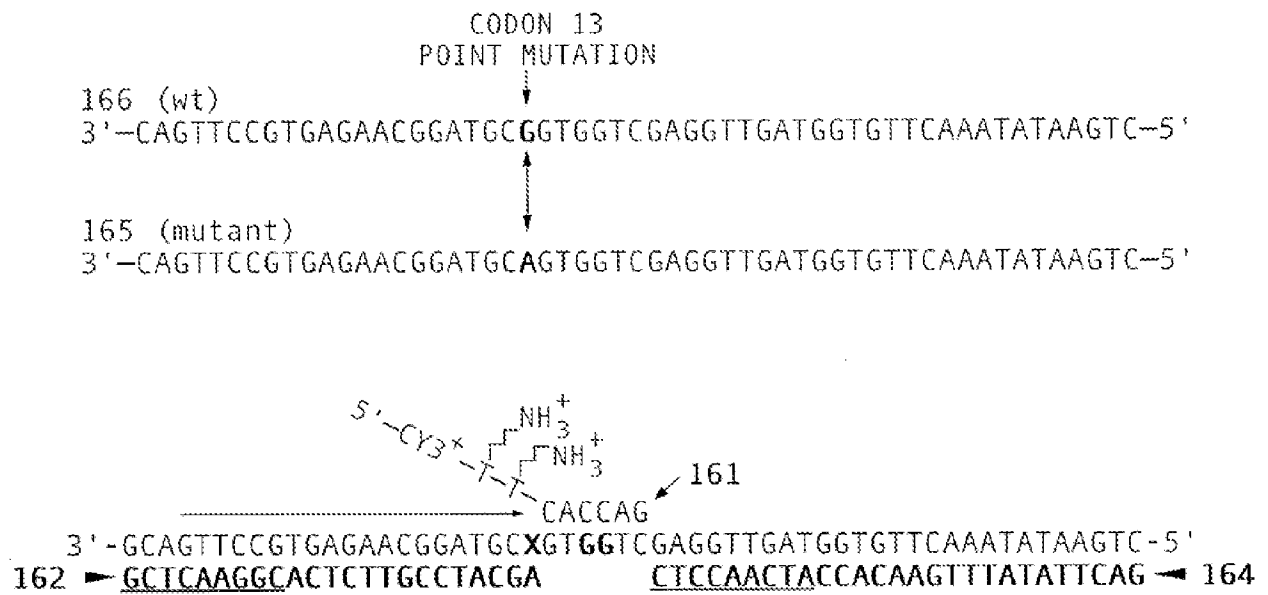


FIGURE 88

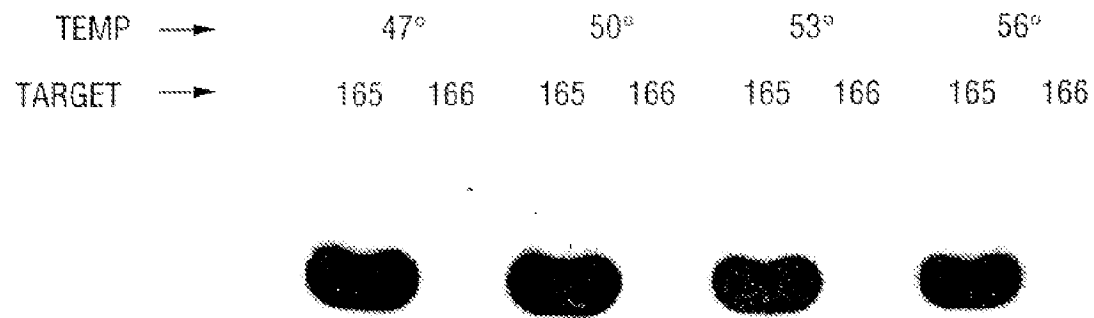


FIGURE 89

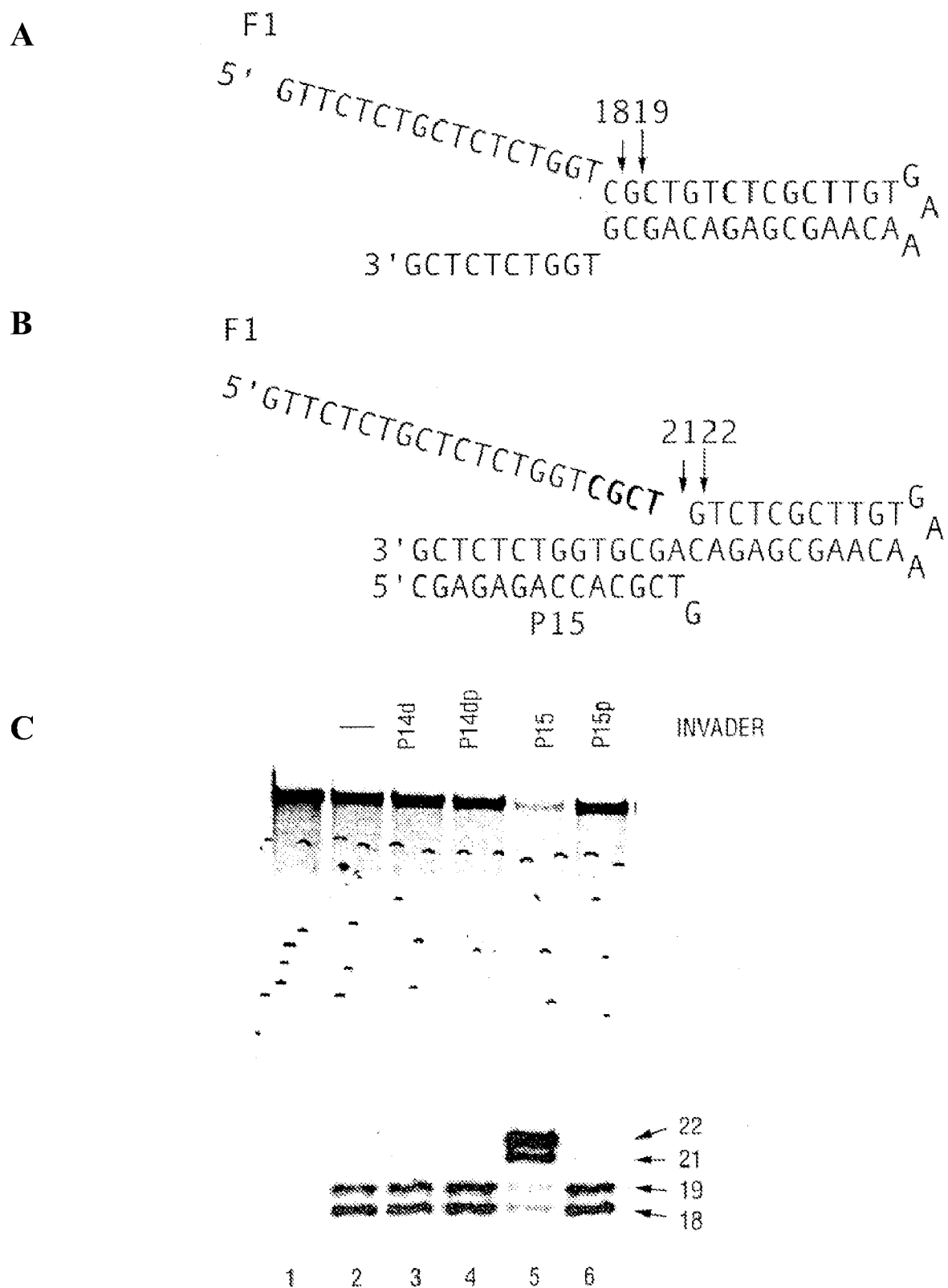


FIGURE 90

## Invader 3' -end Substituents

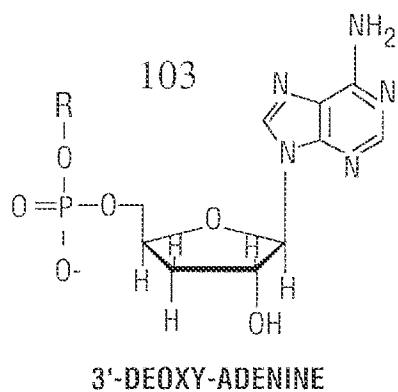
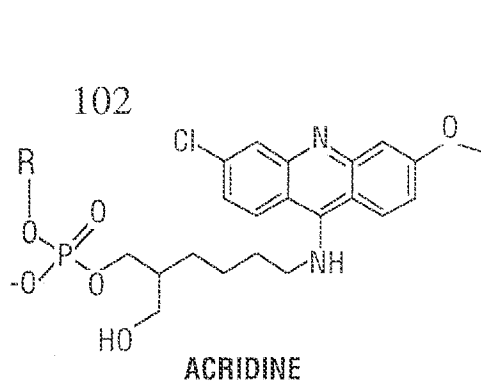
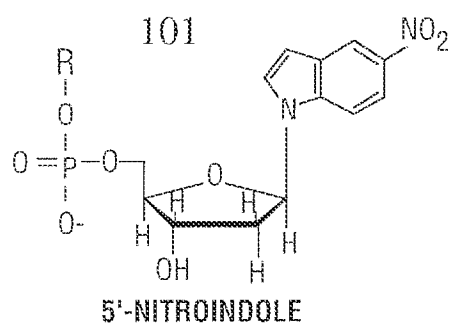
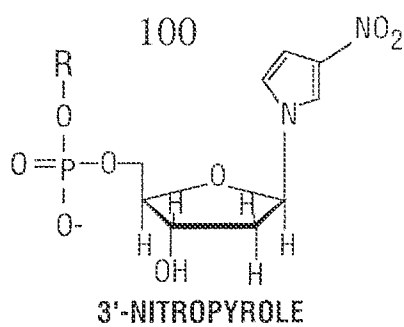
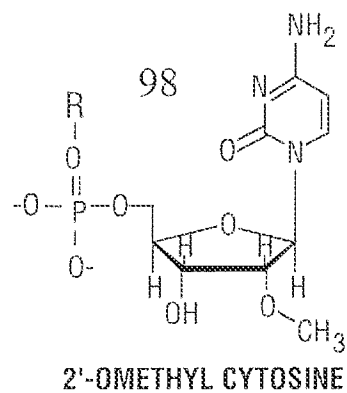
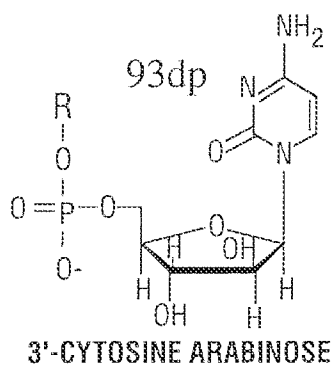
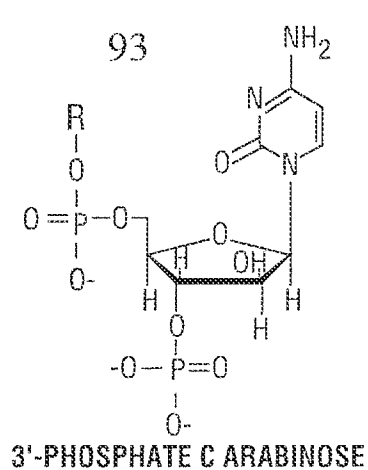
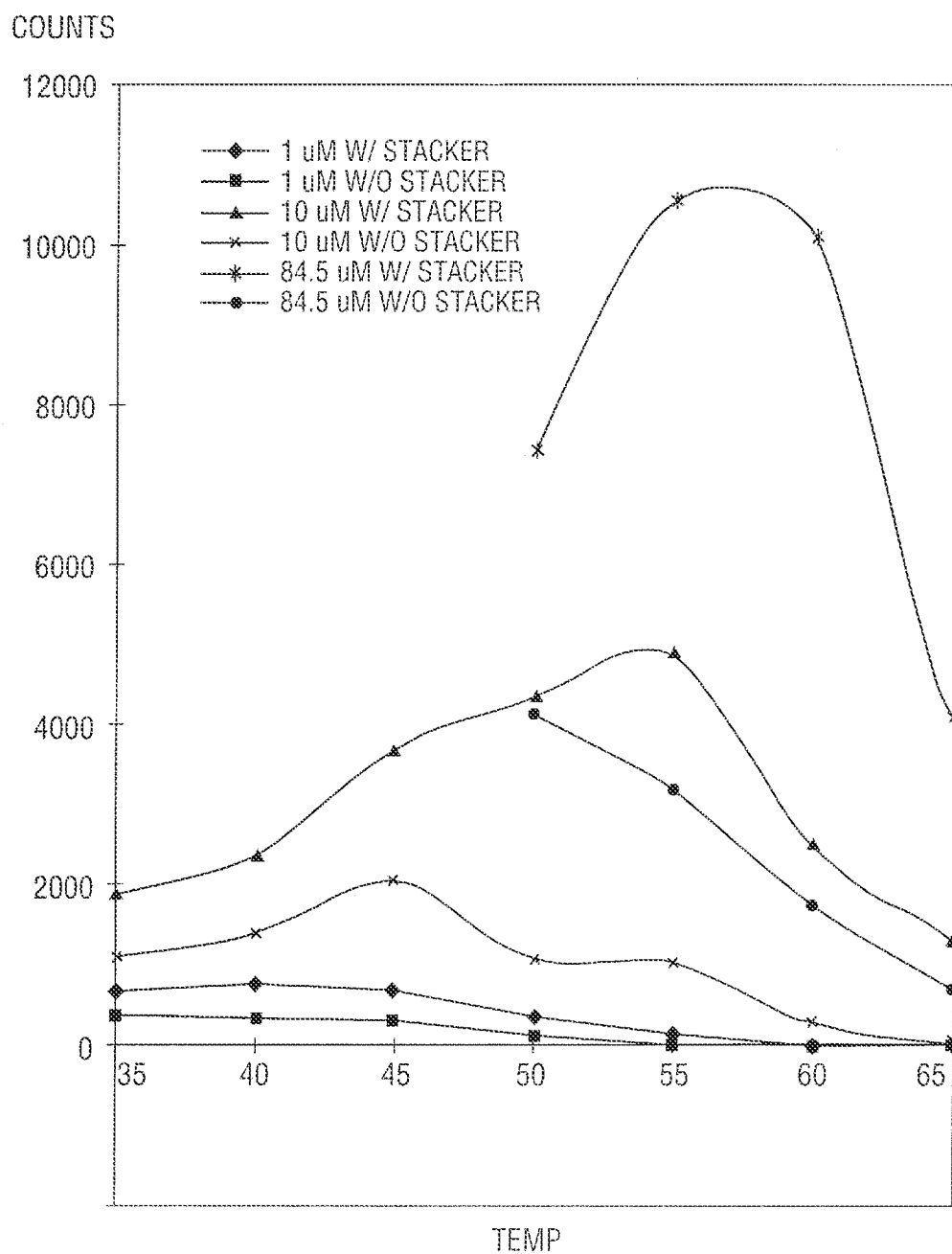
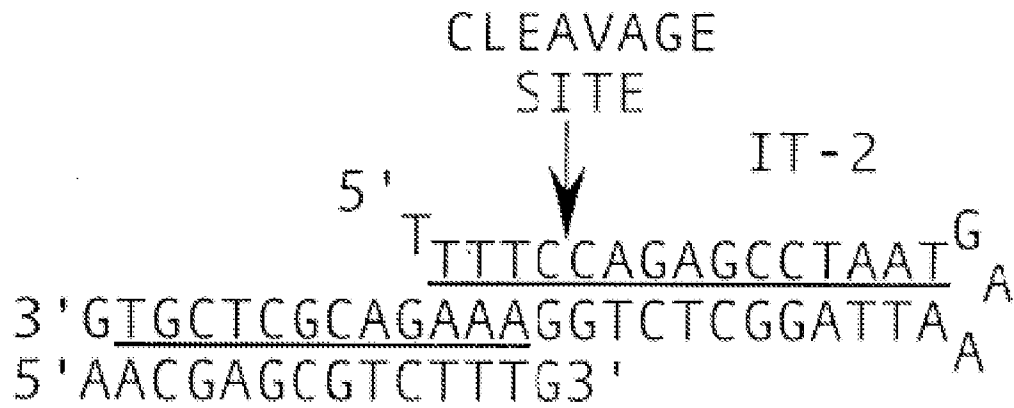


FIGURE 91

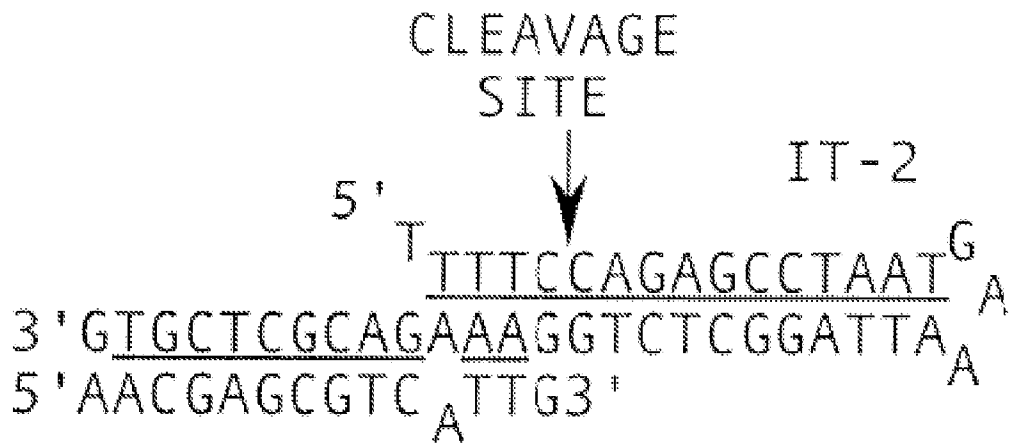


CONCENTRATION OF PROBE W/ AND W/O STACKER vs TEMP

FIGURE 92



IT-1



IT-1A4

FIGURE 93

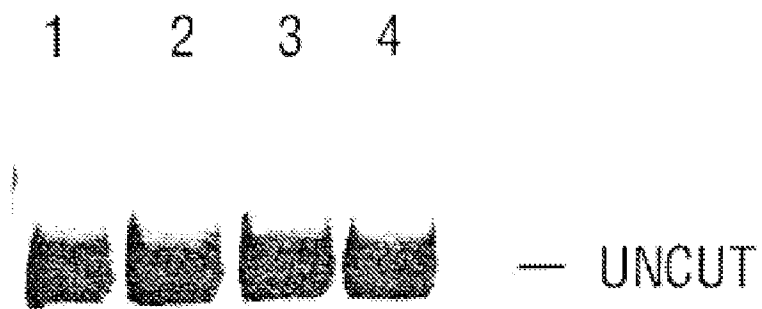


FIGURE 94

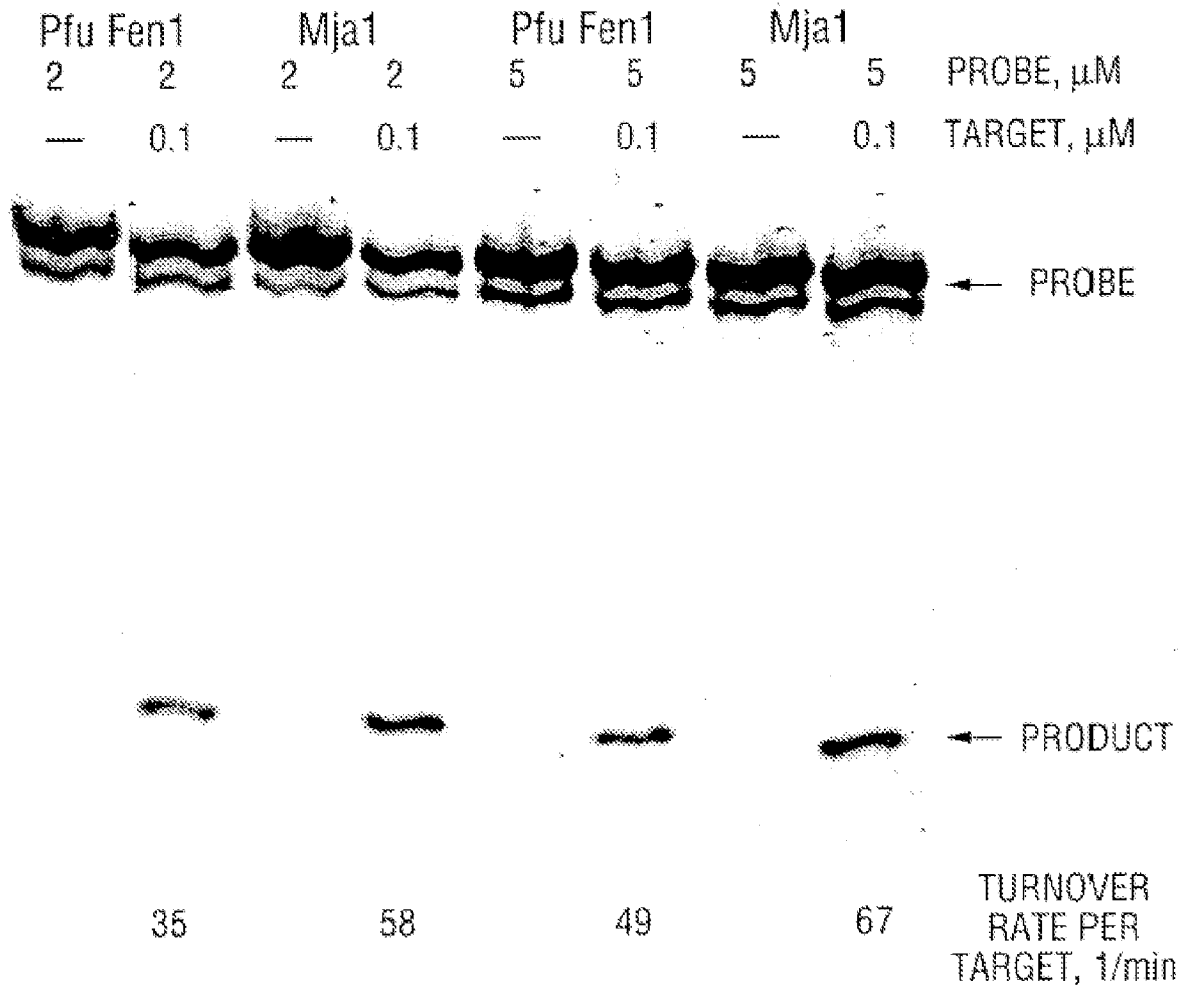
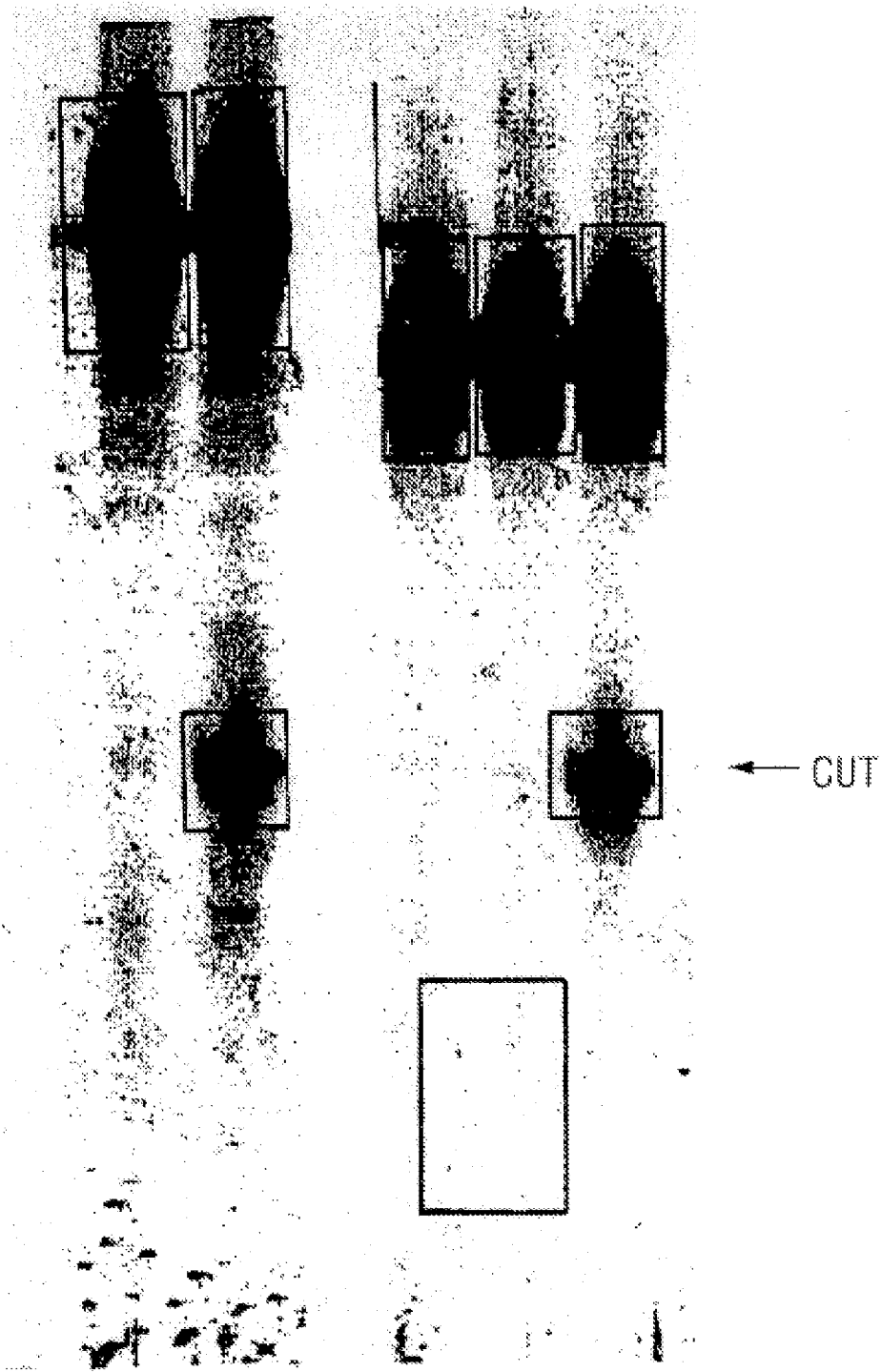
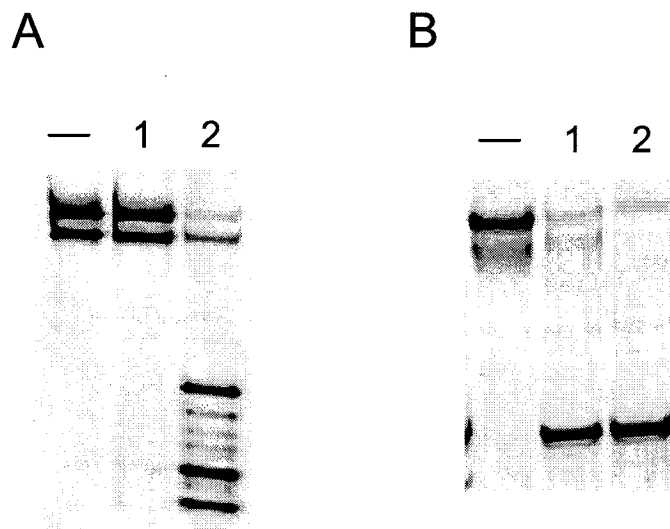




FIGURE 95

1 2 3 4 5



**FIGURE 96**

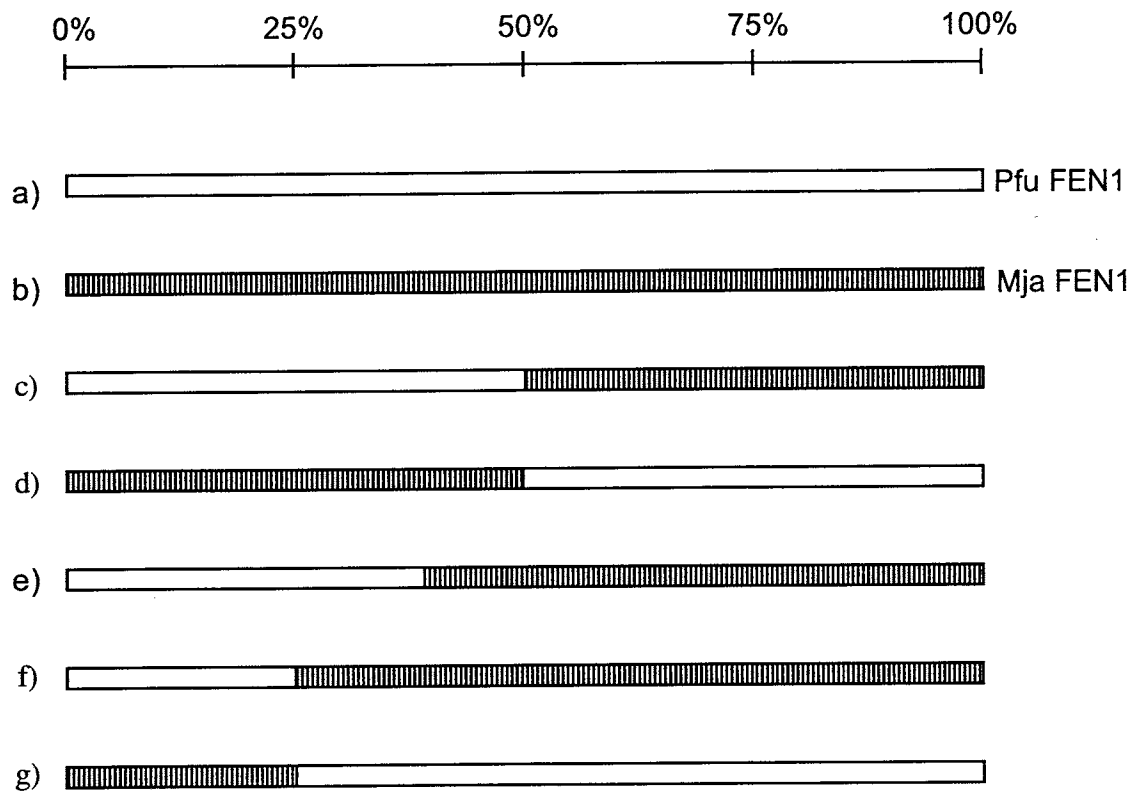
**FIGURE 97**

FIGURE 98A

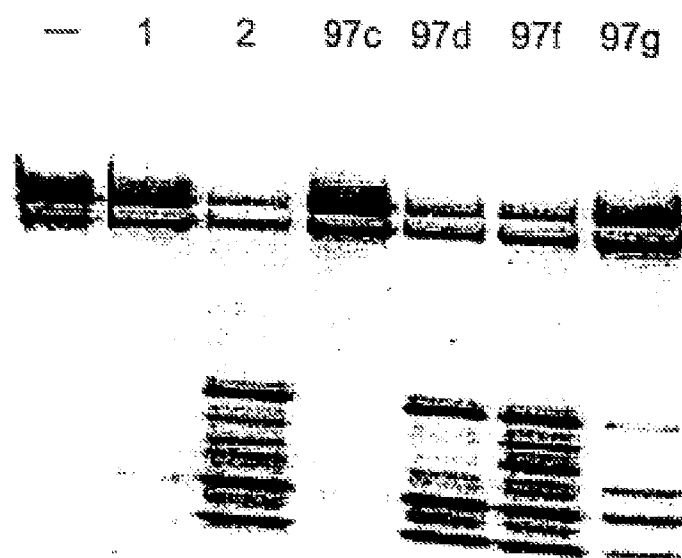


FIGURE 98B

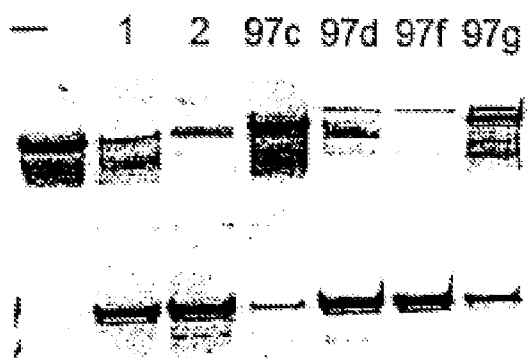
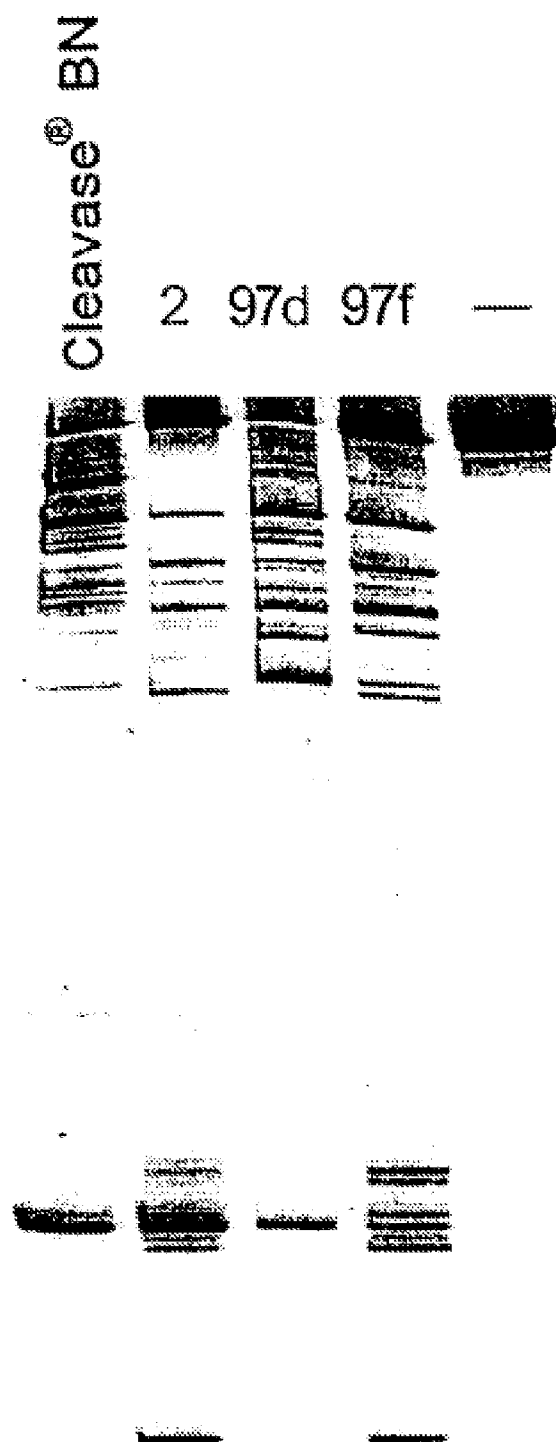
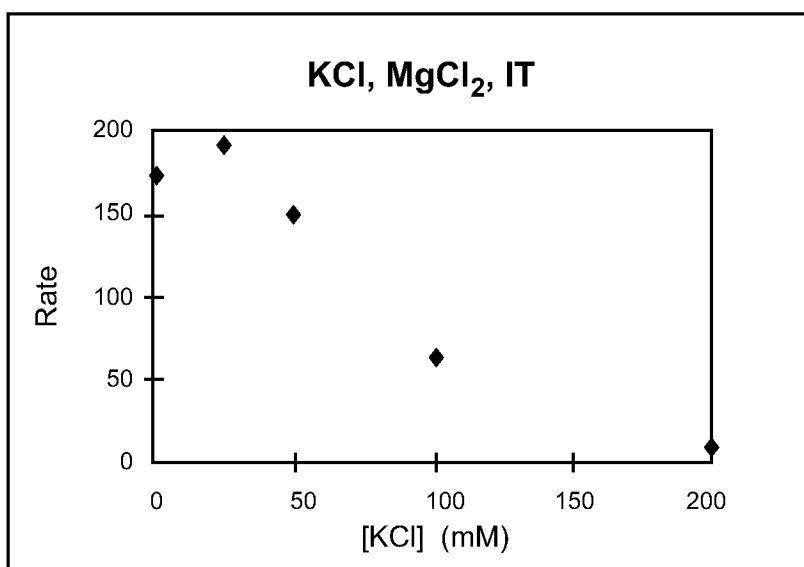
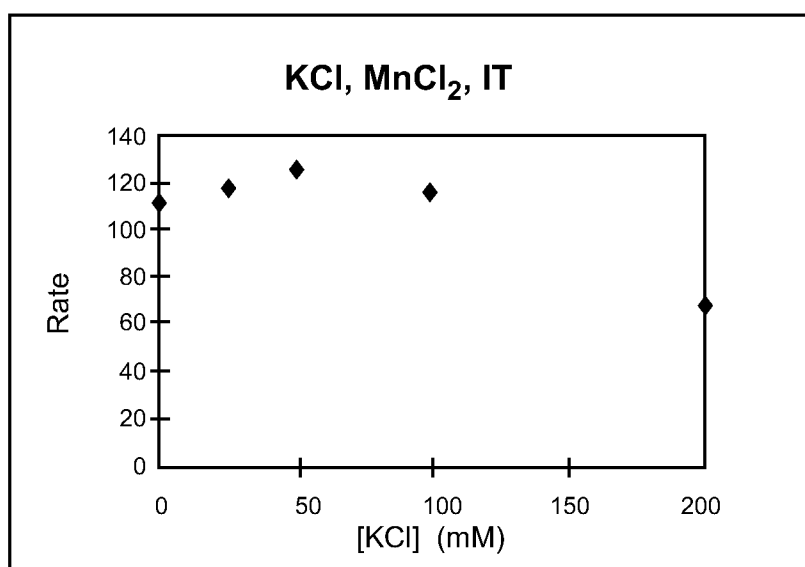


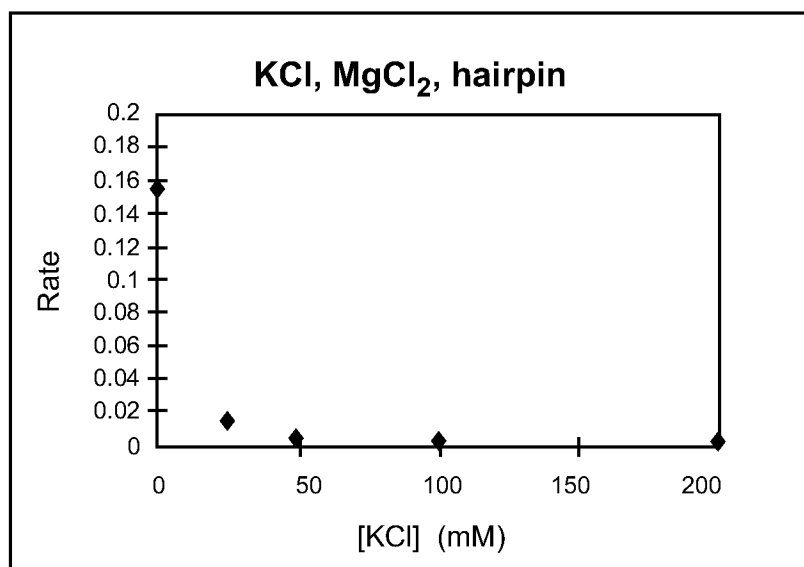
FIGURE 99

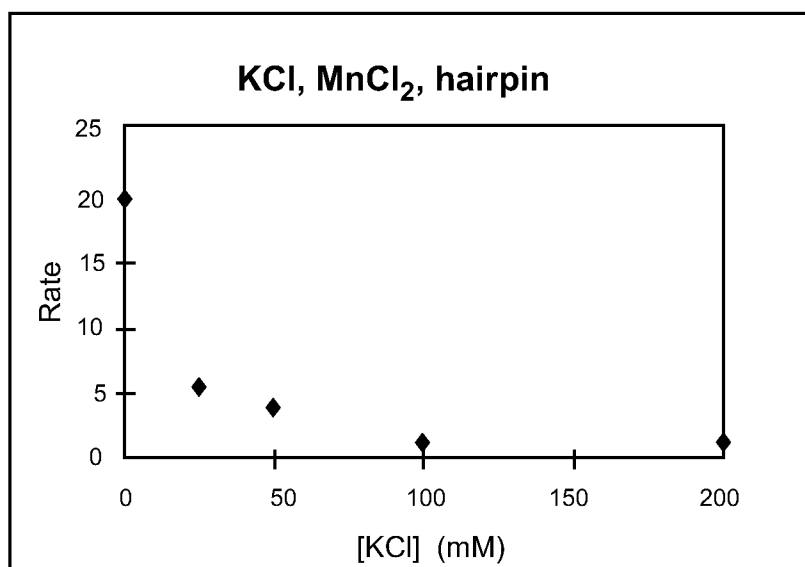


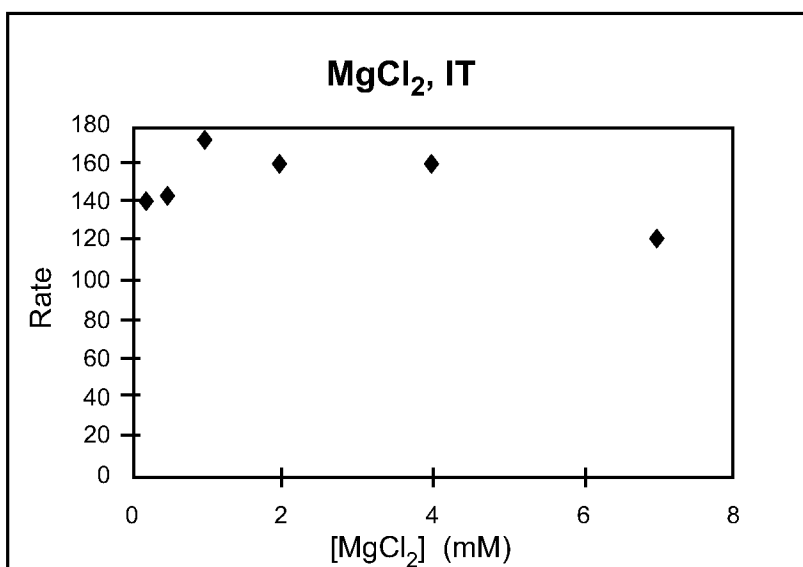
**FIG. 100A**

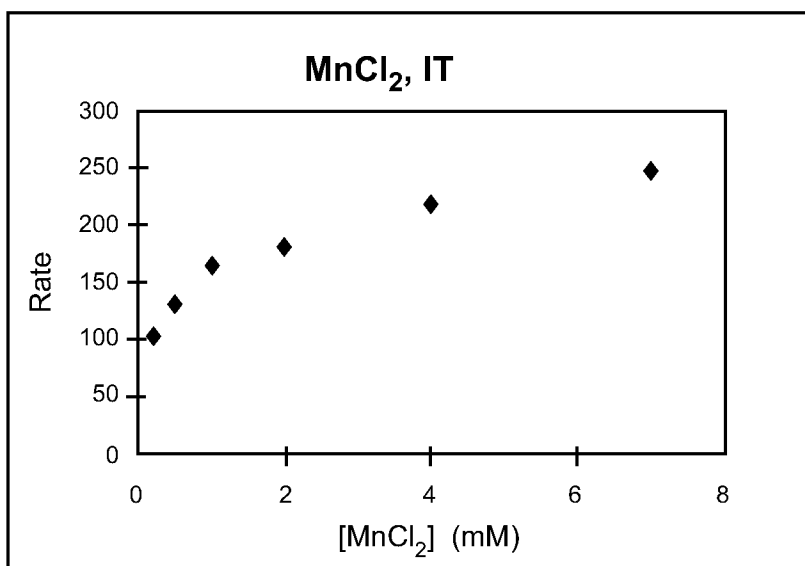
**FIG. 100B**

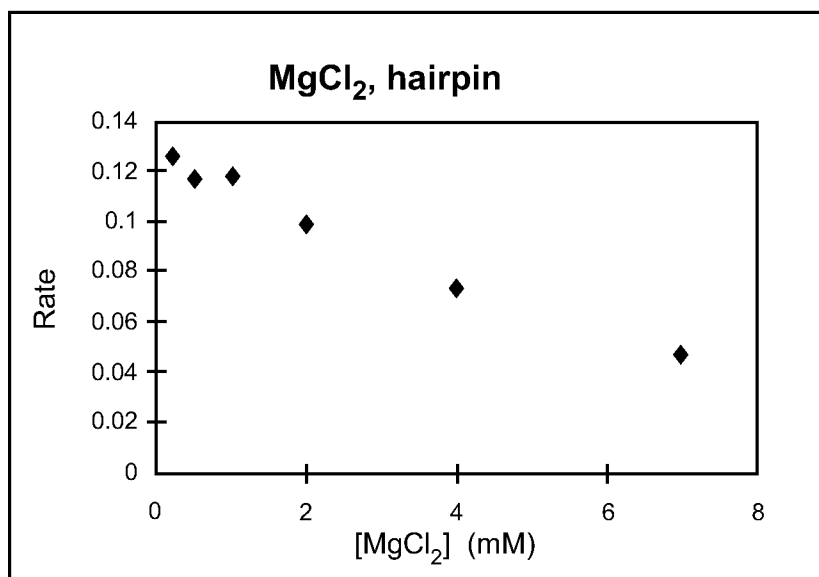


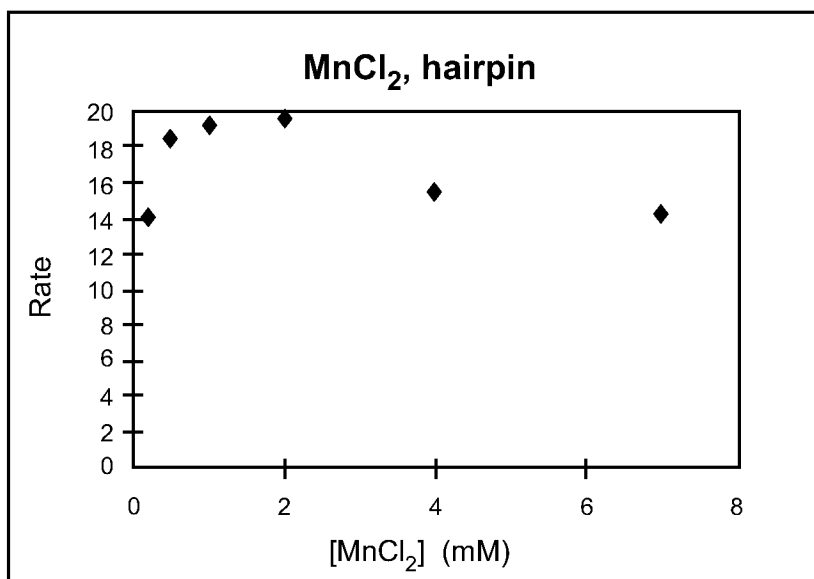
**FIG. 100C**

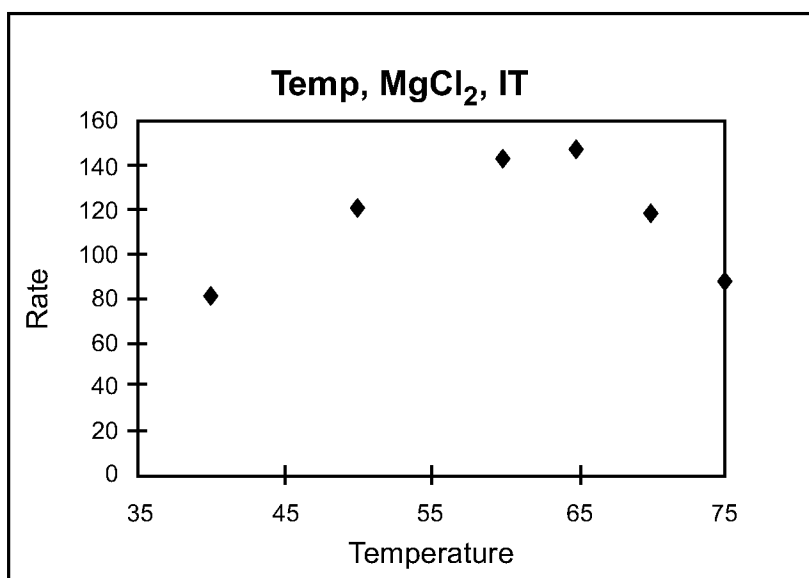
**FIG. 100D**

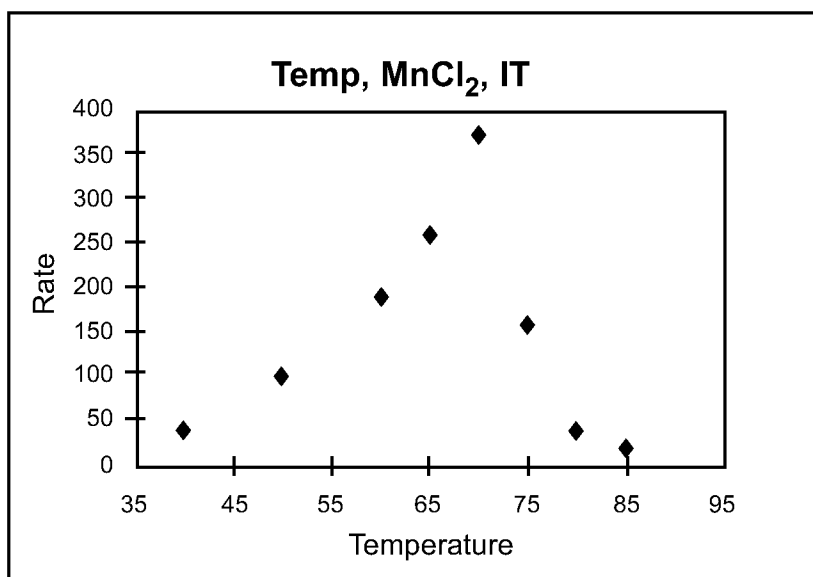
**FIG. 100E**

**FIG. 100F**

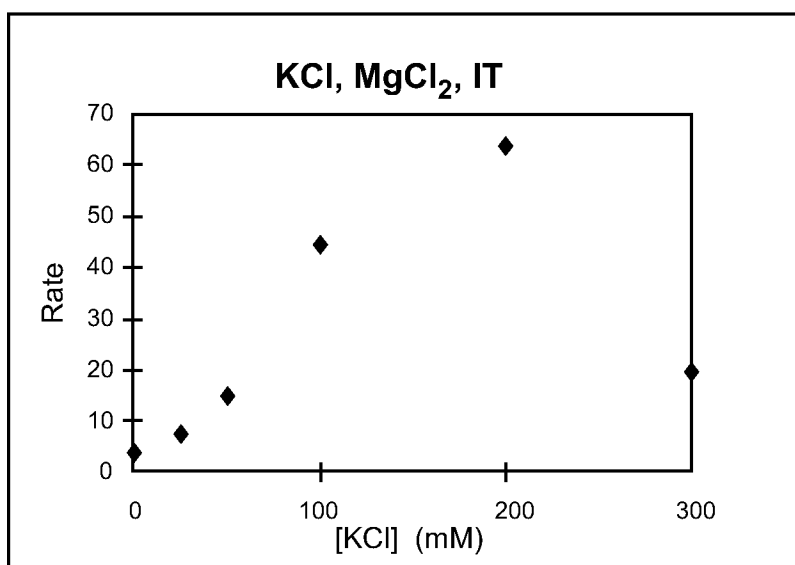
**FIG. 100G**

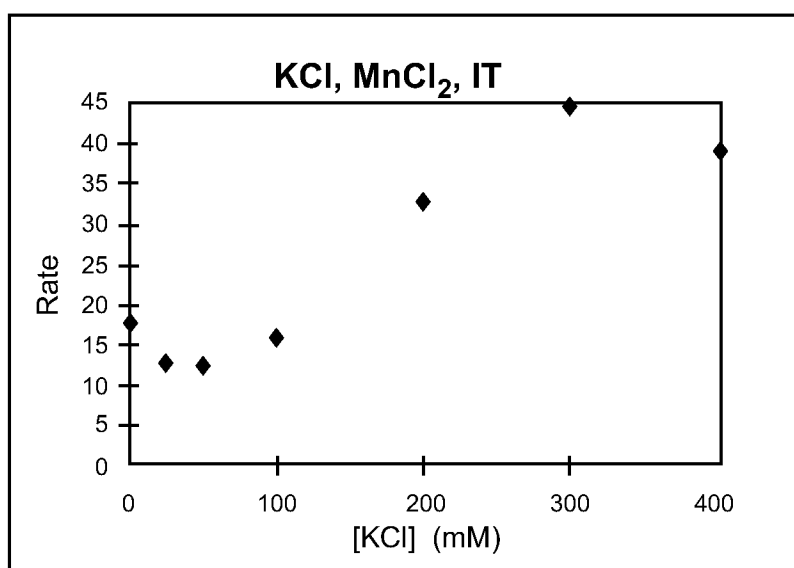
**FIG. 100H**

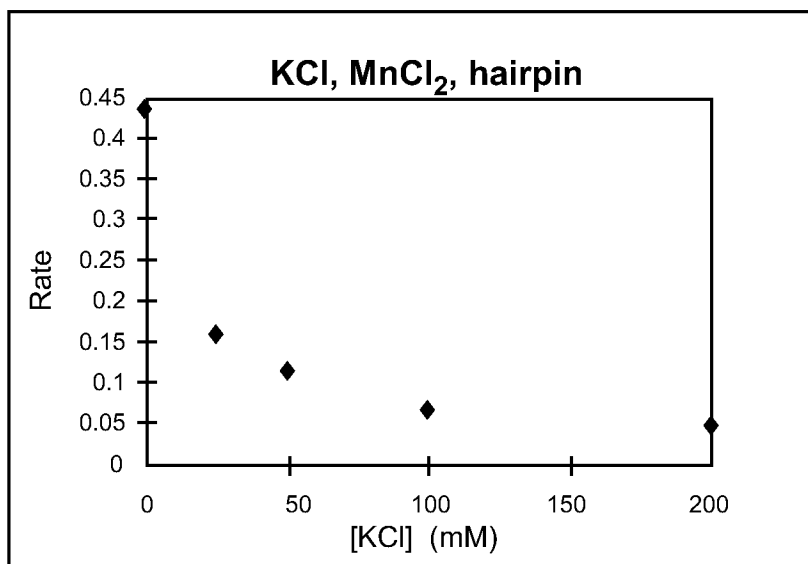
**FIG. 100I**

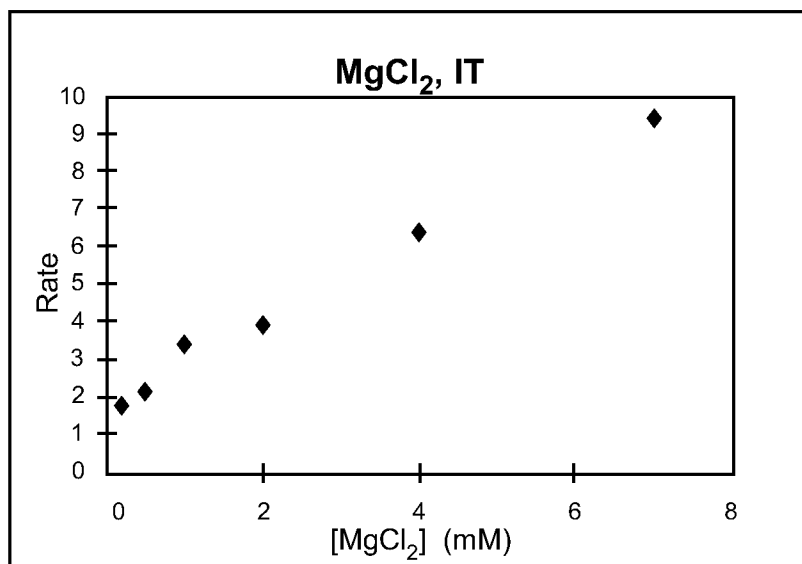
**FIG. 100J**

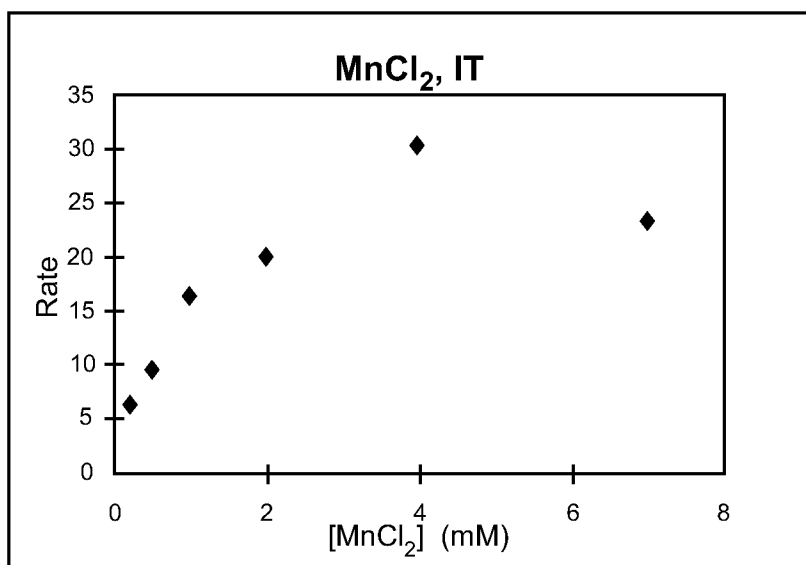


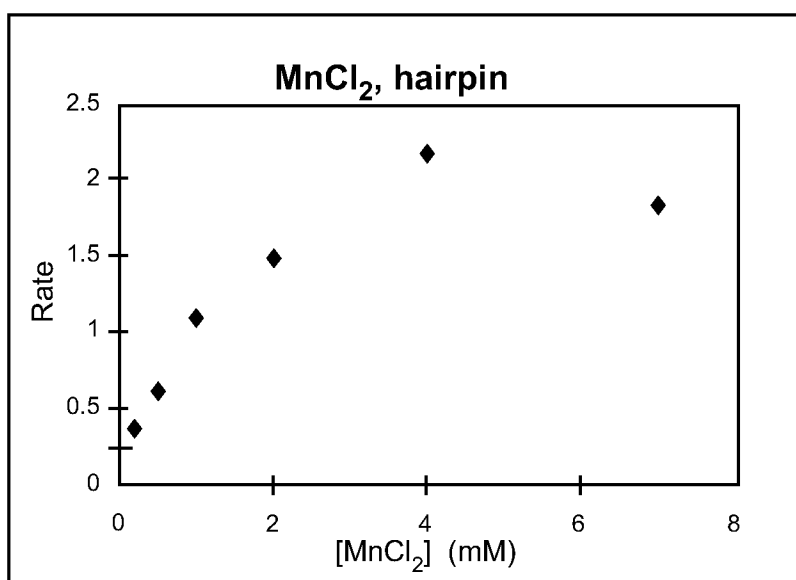
**FIG. 101A**

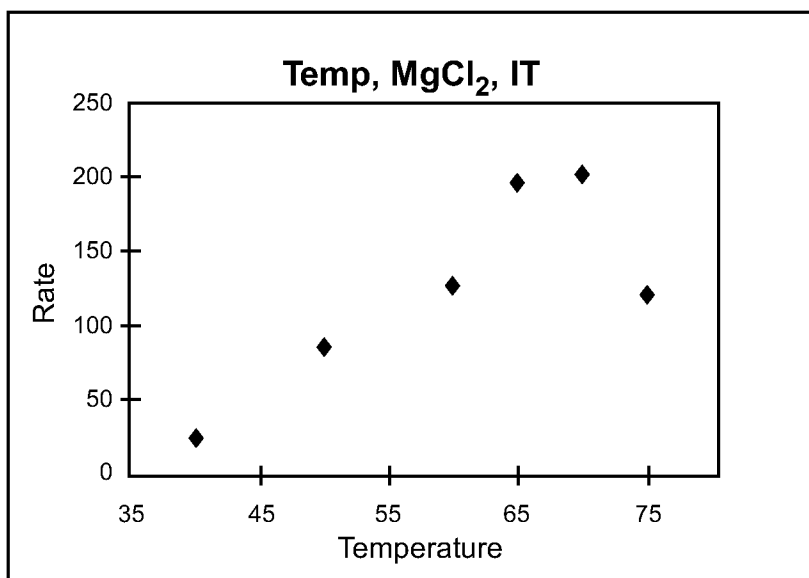
**FIG. 101B**

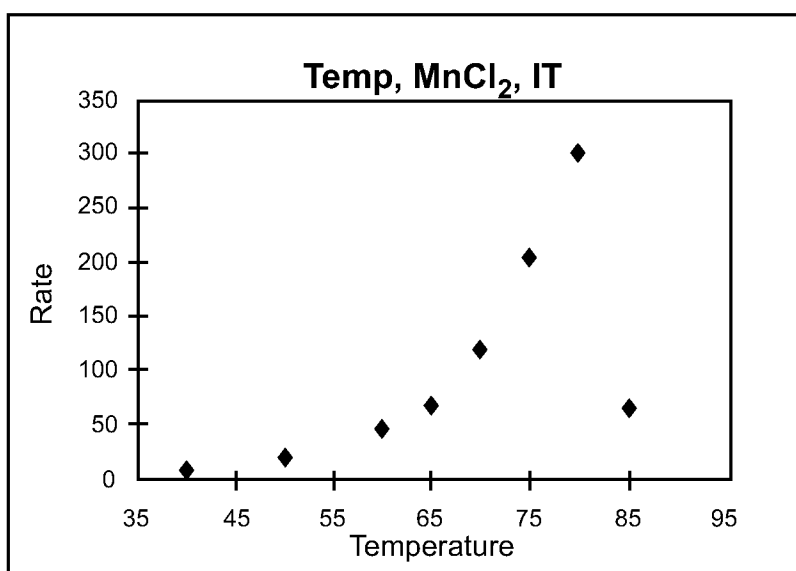
**FIG. 101D**

**FIG. 101E**

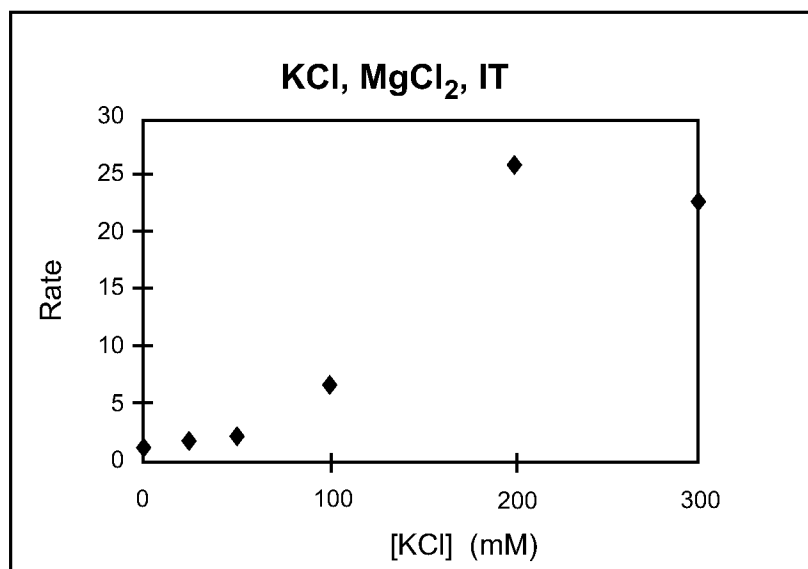
**FIG. 101F**

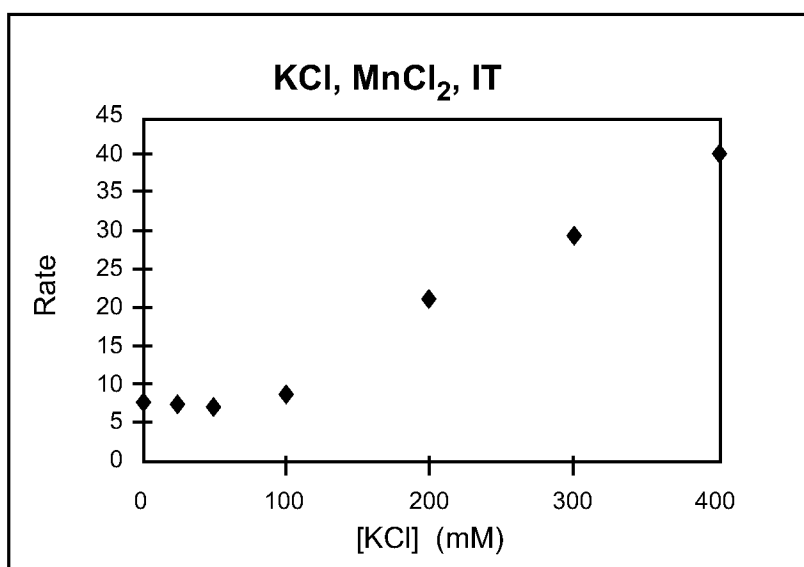
**FIG. 101H**

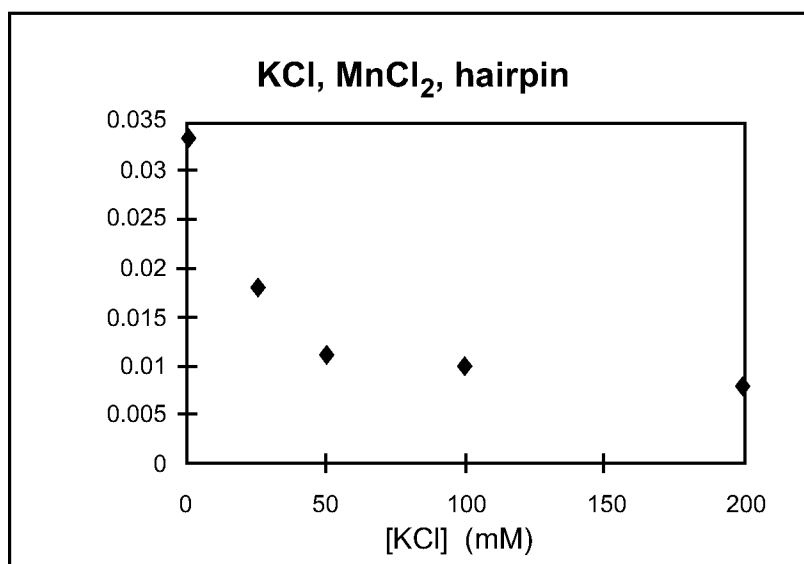
**FIG. 101I**

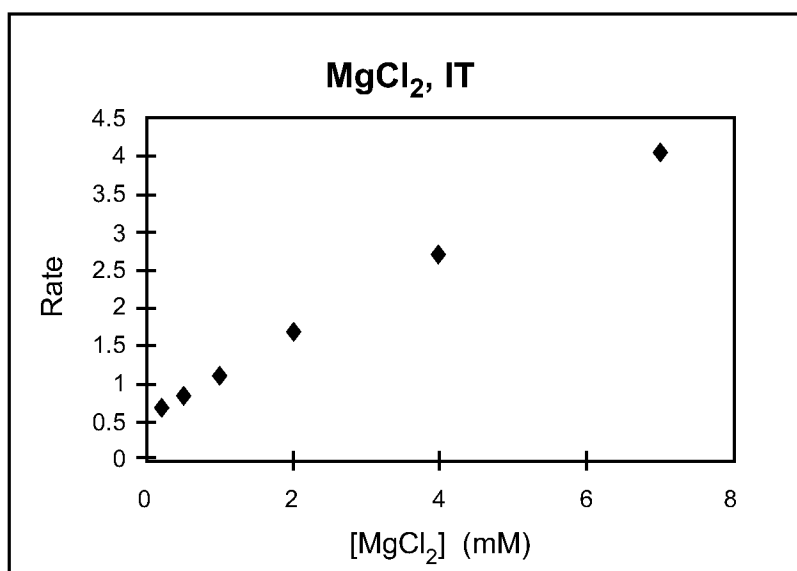
**FIG. 101J**

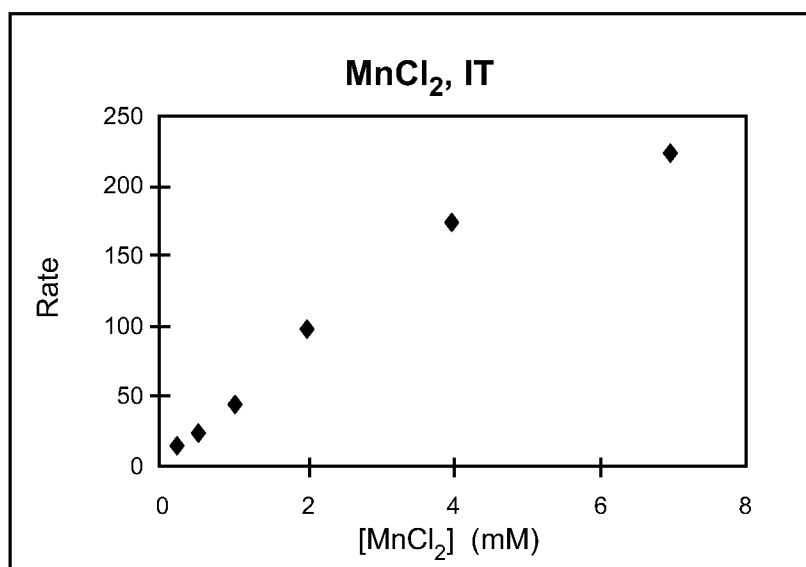


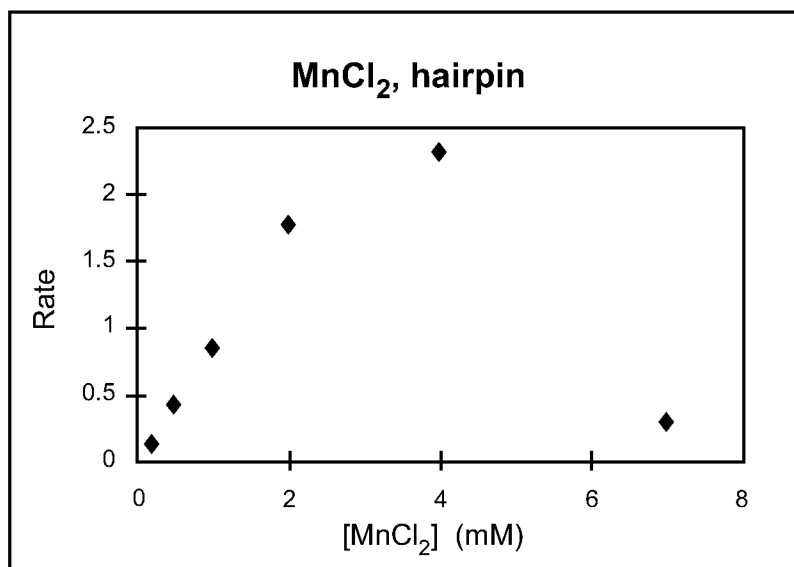
**FIG. 102A**

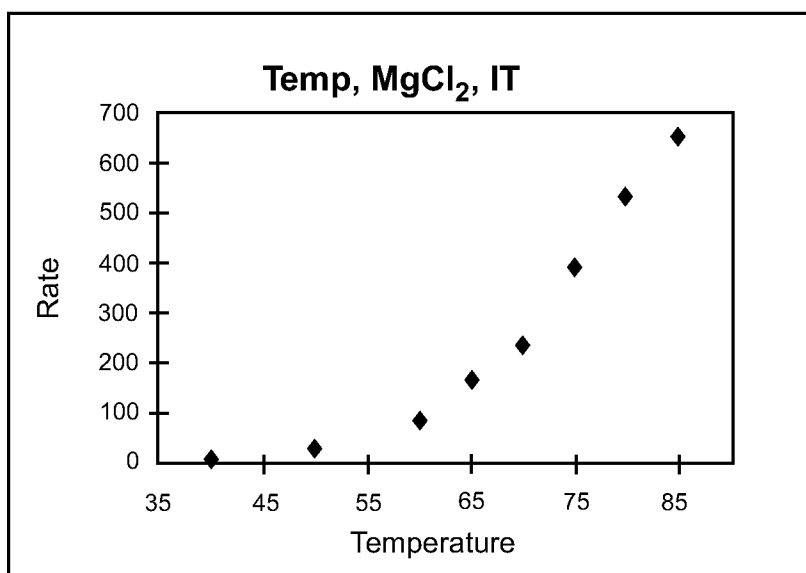
**FIG. 102B**

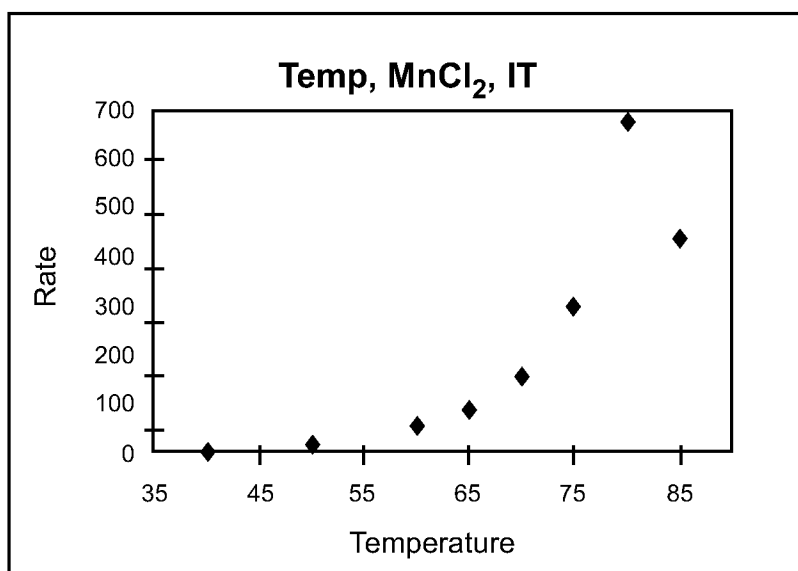
**FIG. 102D**

**FIG. 102E**

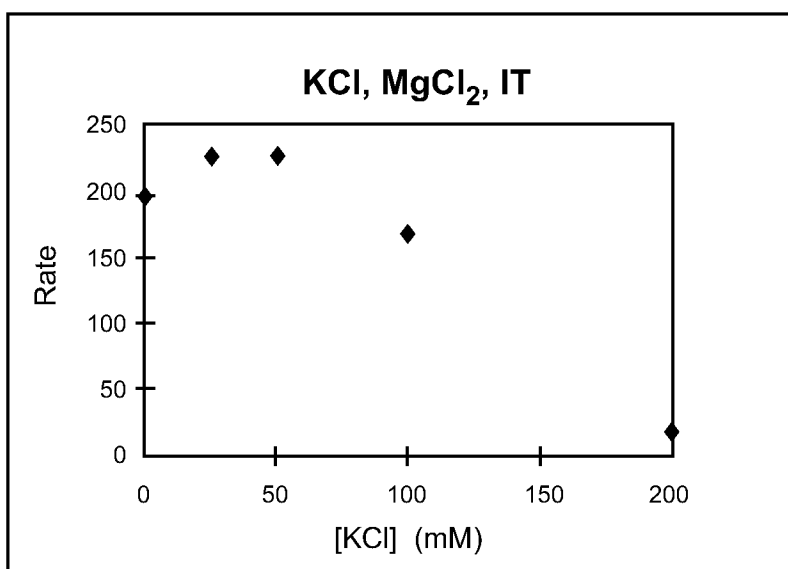
**FIG. 102F**

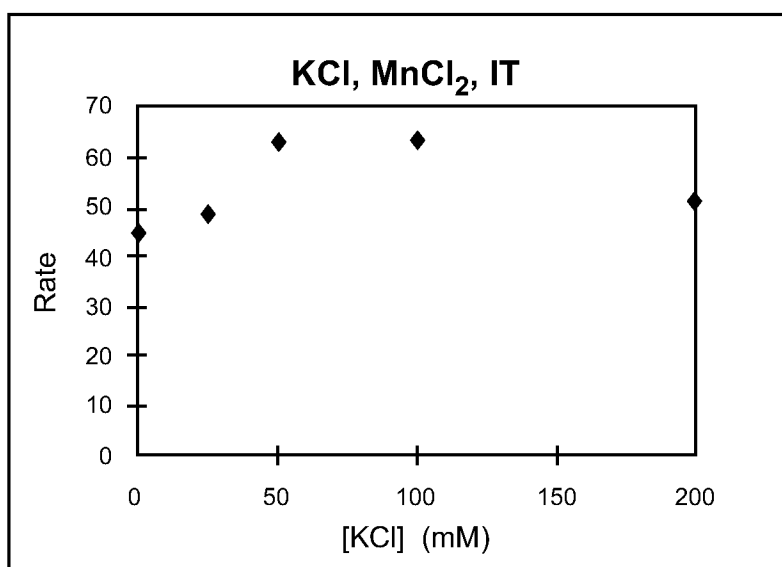
**FIG. 102H**

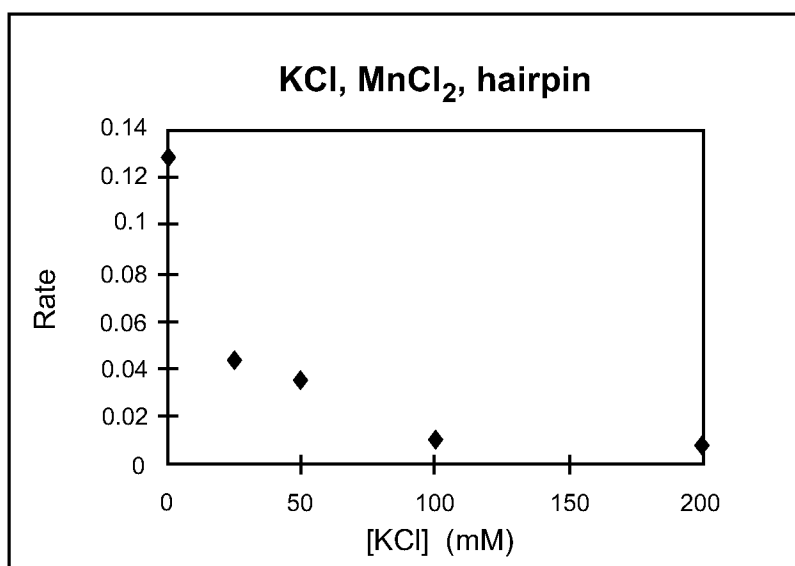
**FIG. 102I**

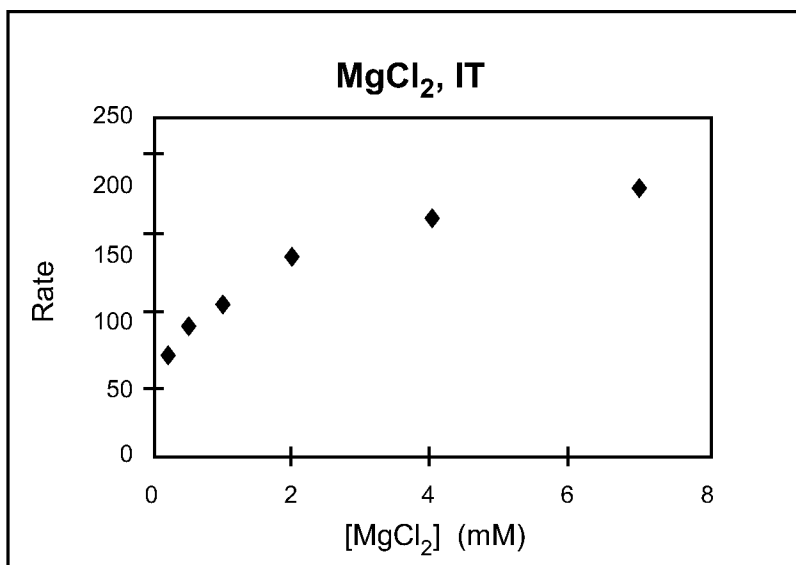
**FIG. 102J**

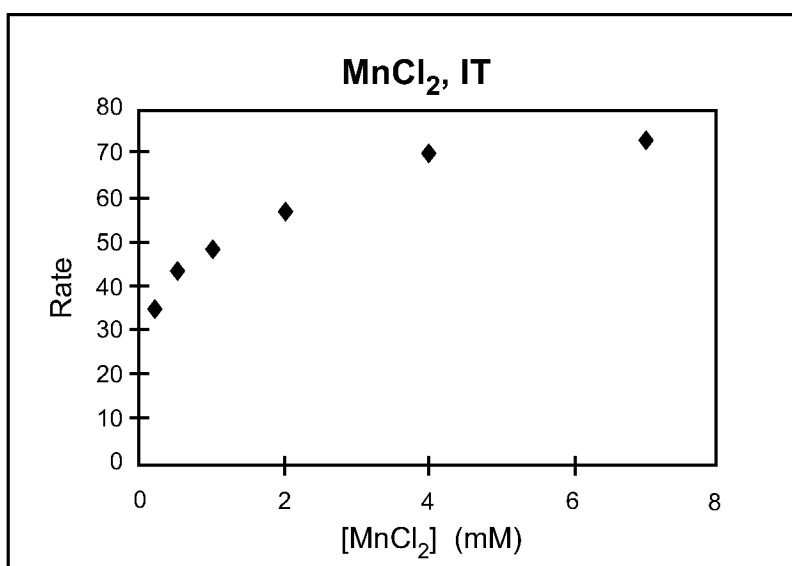


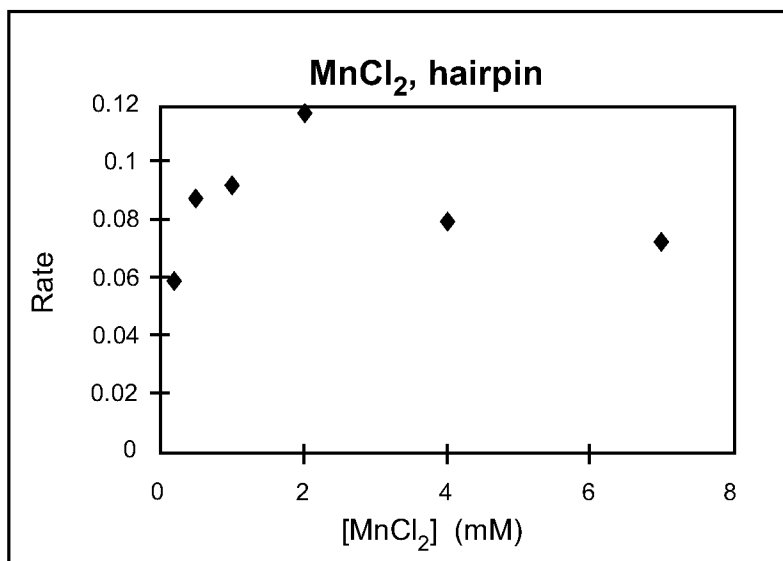
**FIG. 103A**

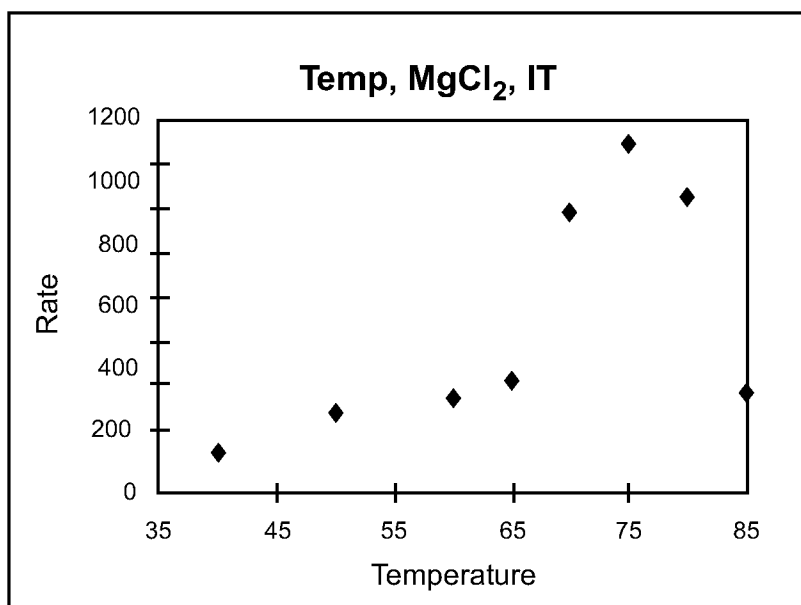
**FIG. 103B**

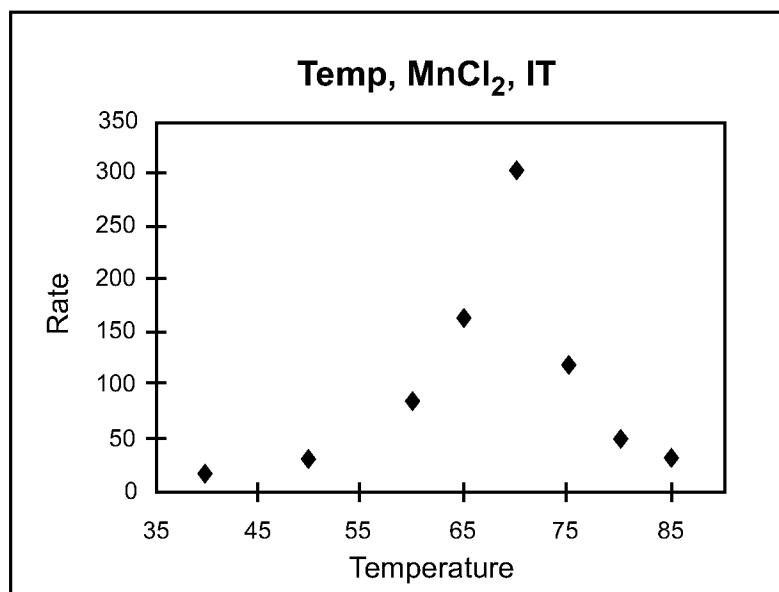
**FIG. 103D**

**FIG. 103E**

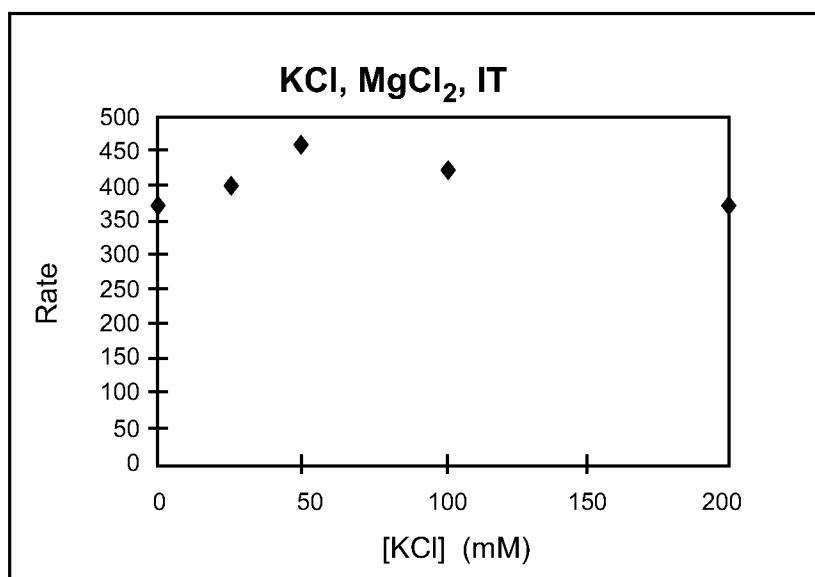
**FIG. 103F**

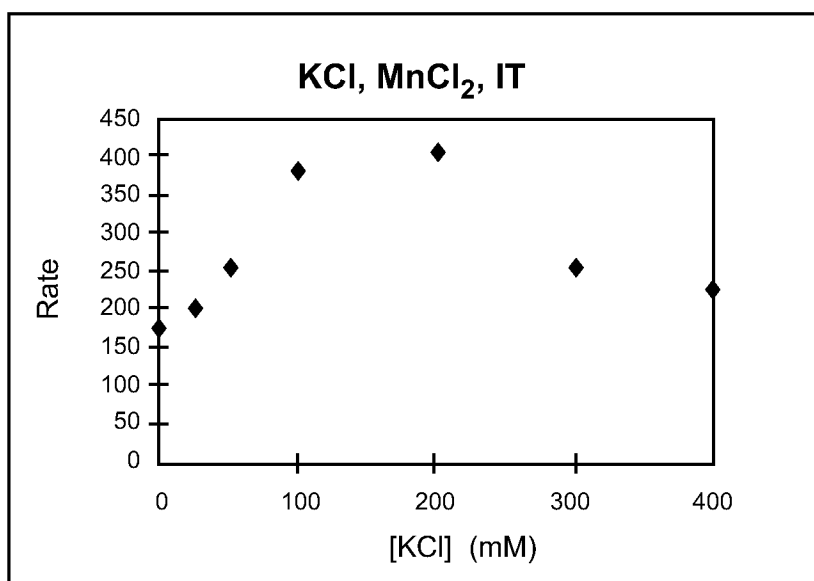
**FIG. 103H**

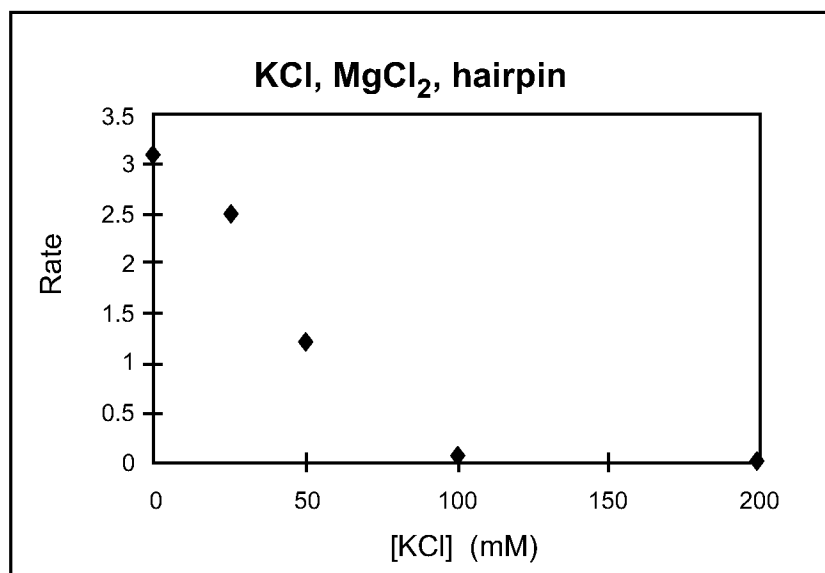
**FIG. 103I**

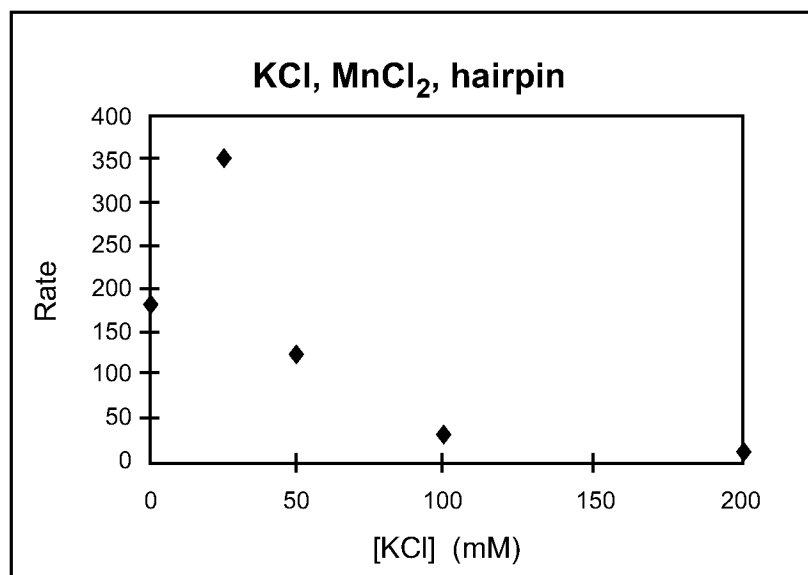
**FIG. 103J**

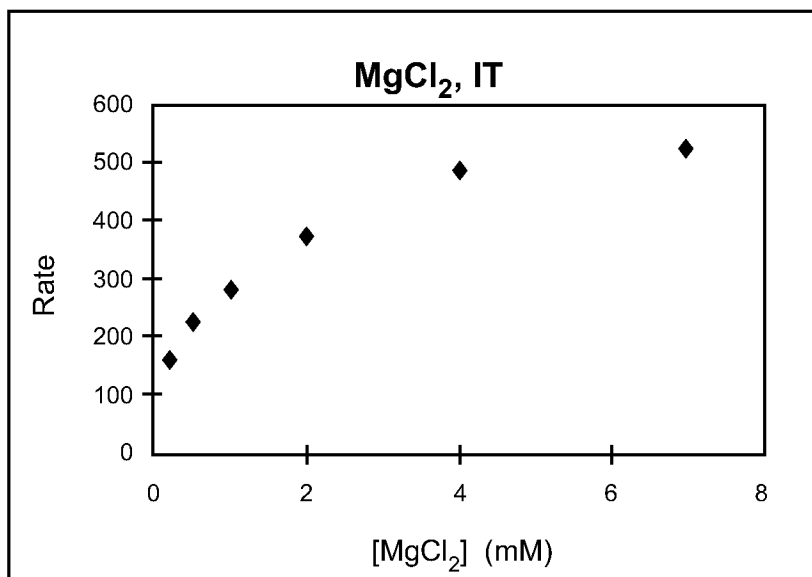


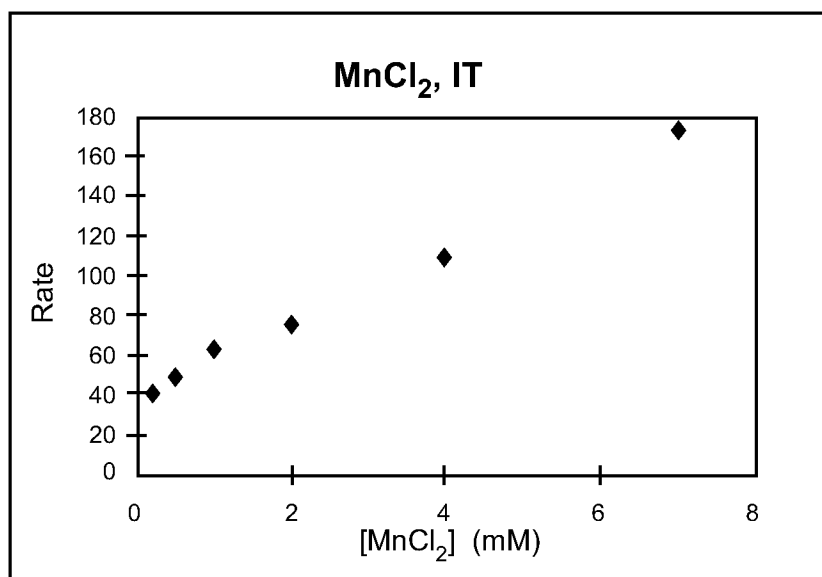
**FIG. 104A**

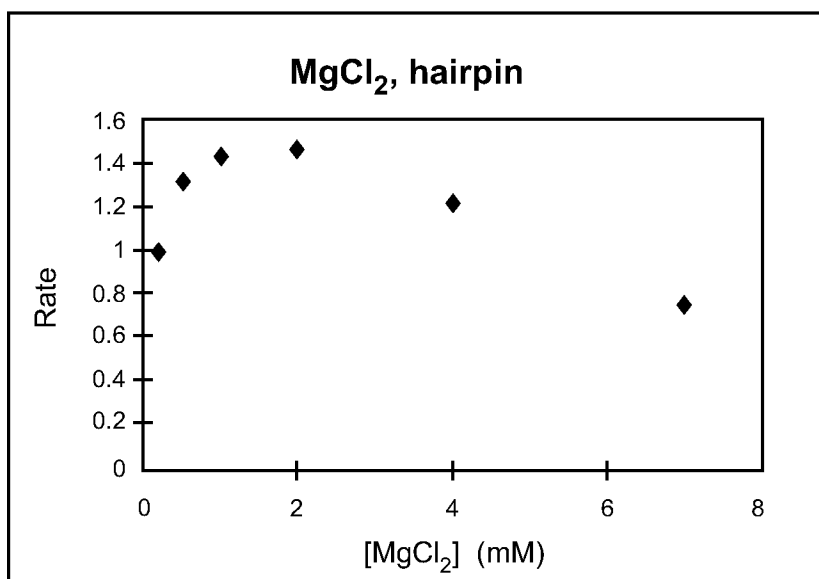
**FIG. 104B**

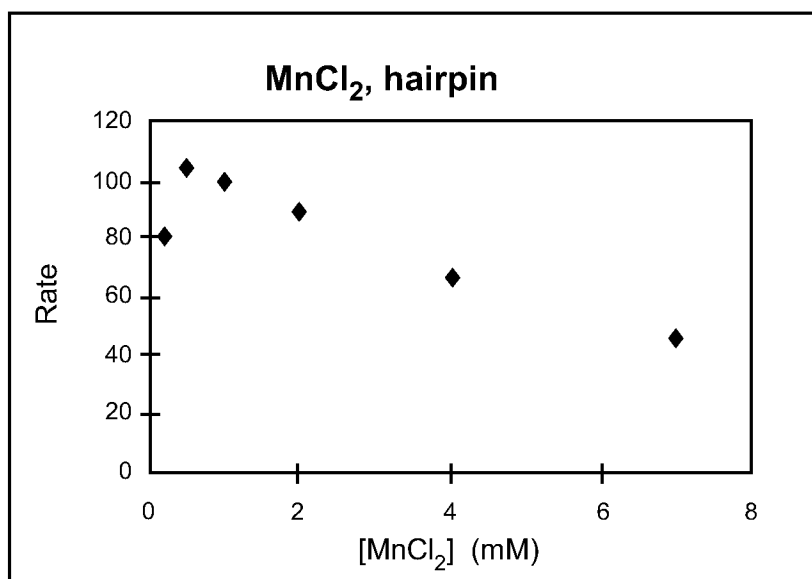
**FIG. 104C**

**FIG. 104D**

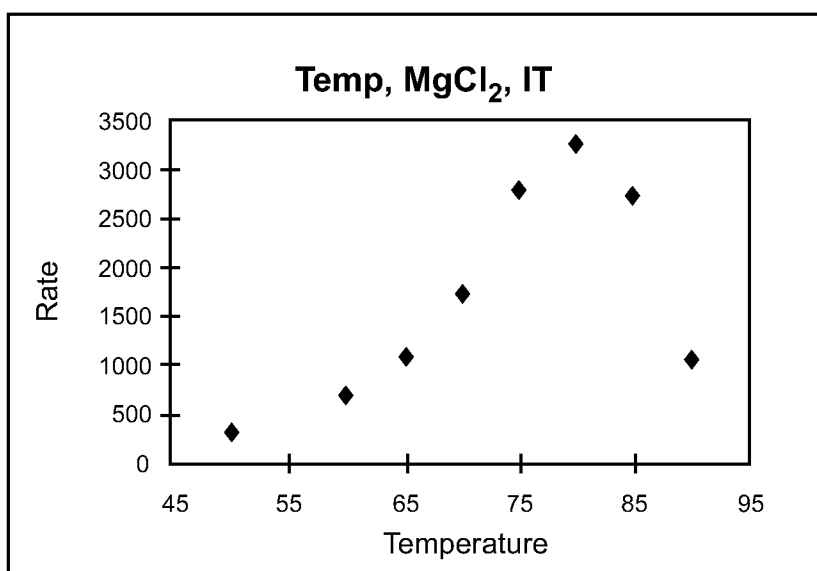
**FIG. 104E**

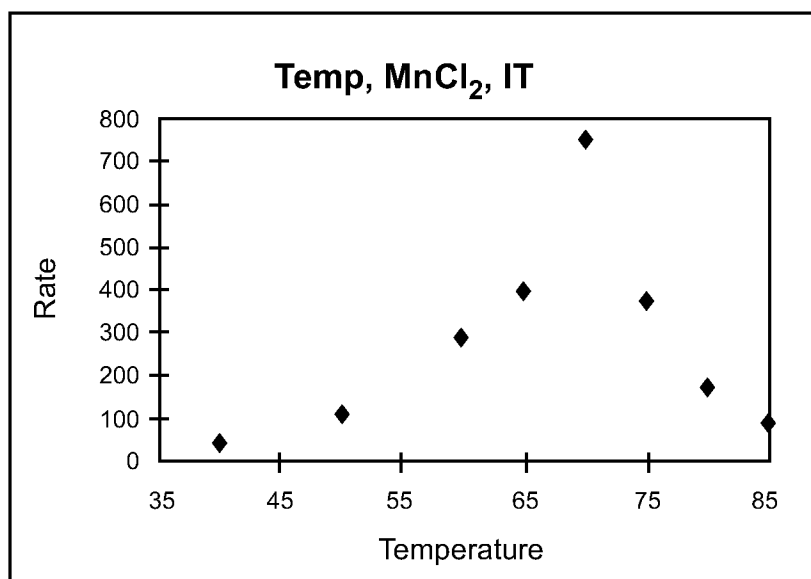
**FIG. 104F**

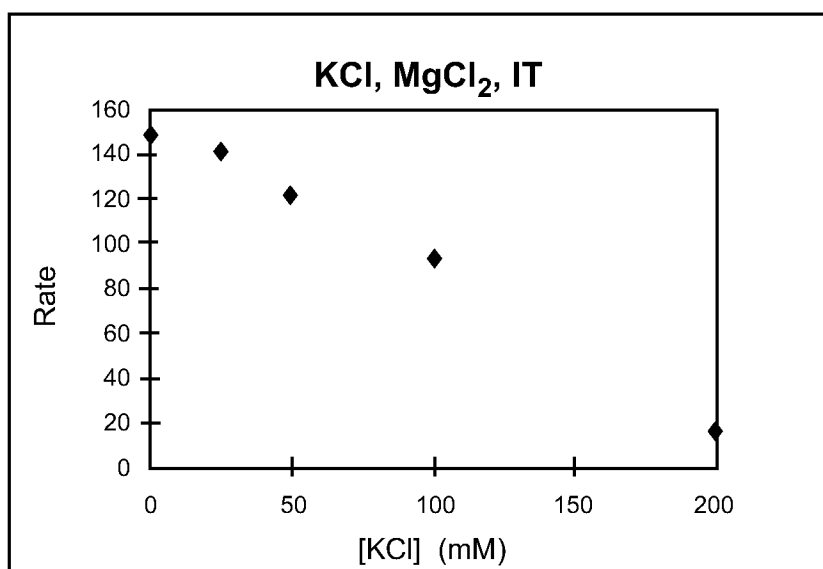
**FIG. 104G**

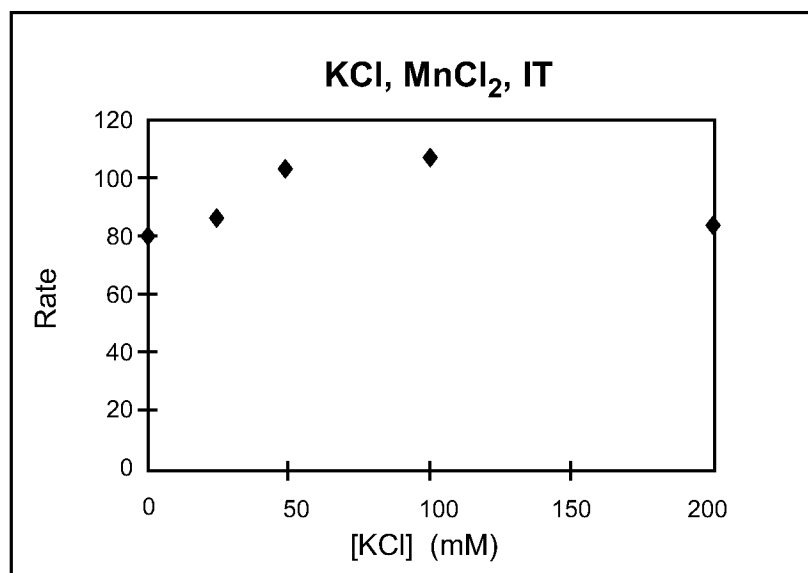
**FIG. 104H**

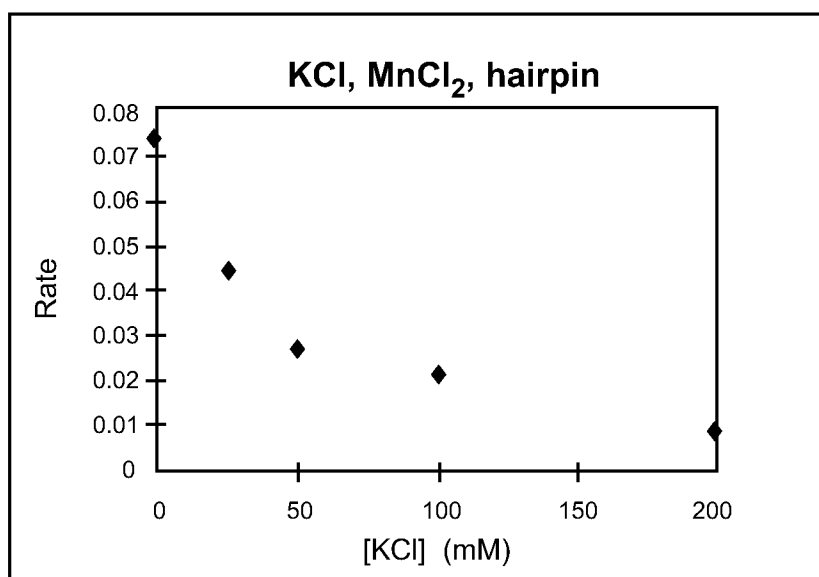


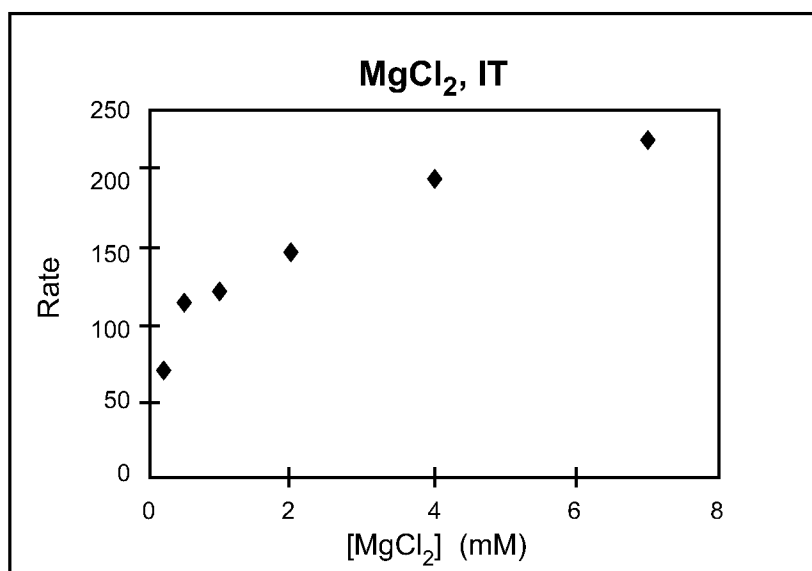
**FIG. 104I**

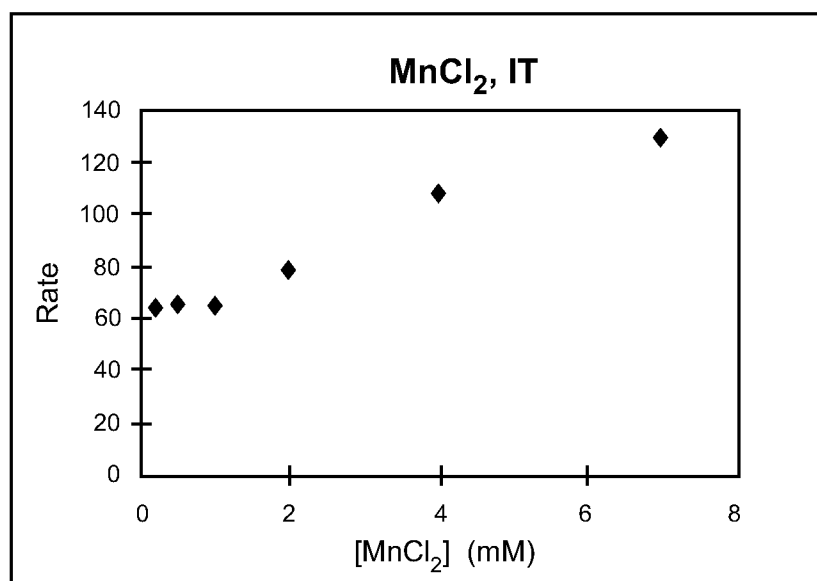
**FIG. 104J**

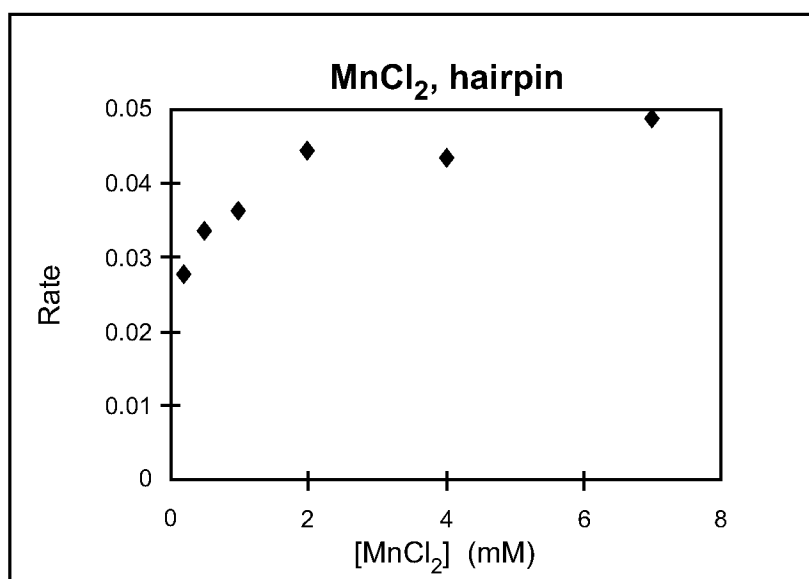
**FIG. 105A**

**FIG. 105B**

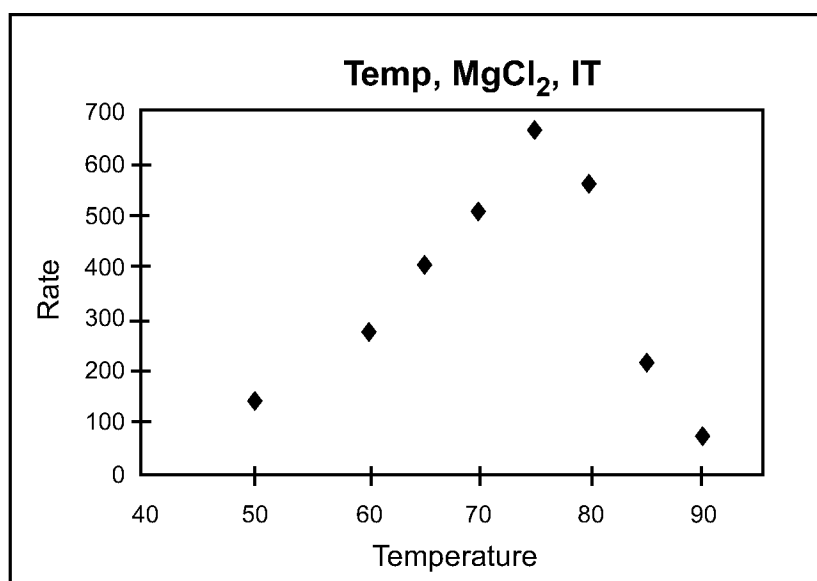
**FIG. 105D**

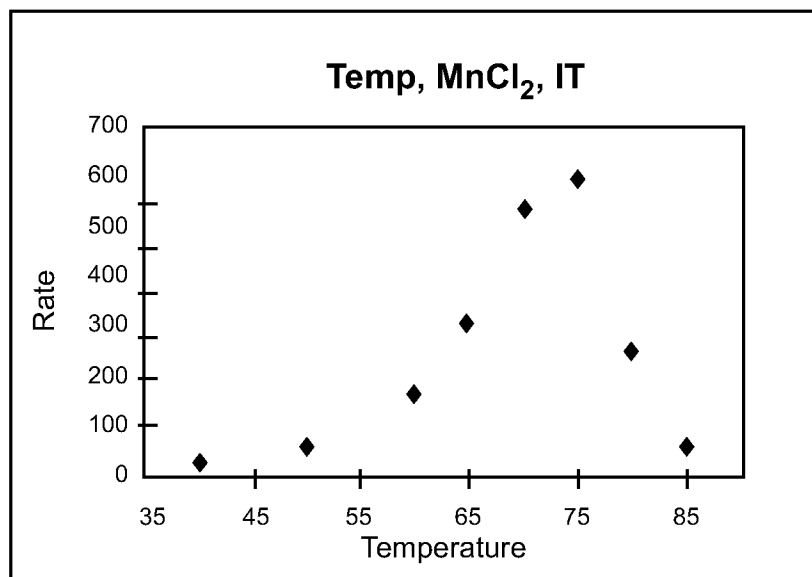
**FIG. 105E**

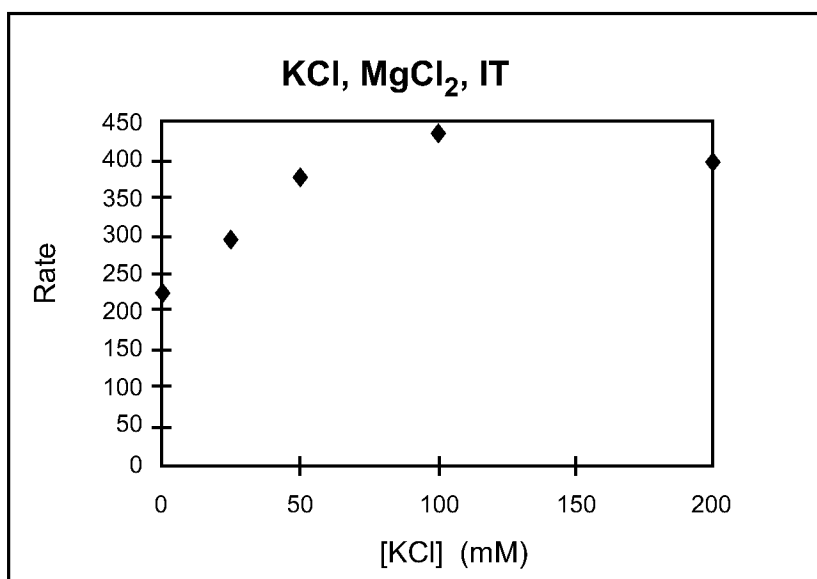
**FIG. 105F**

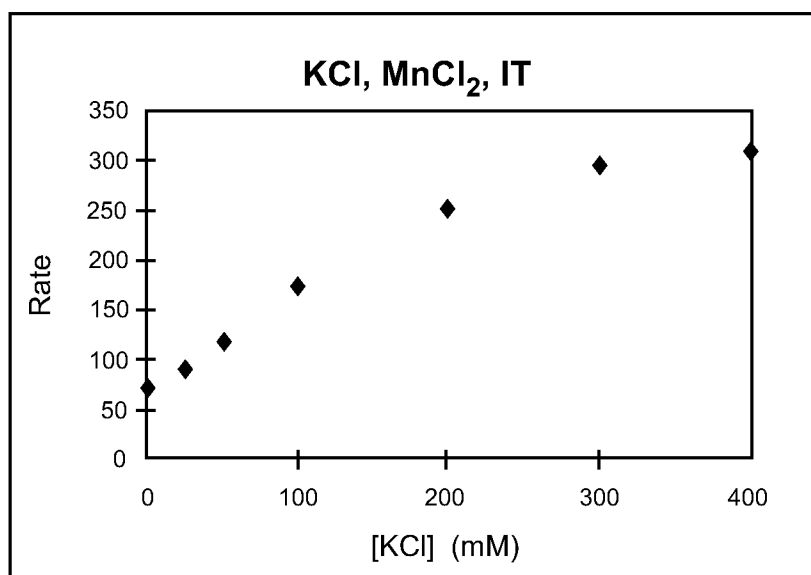
**FIG. 105H**

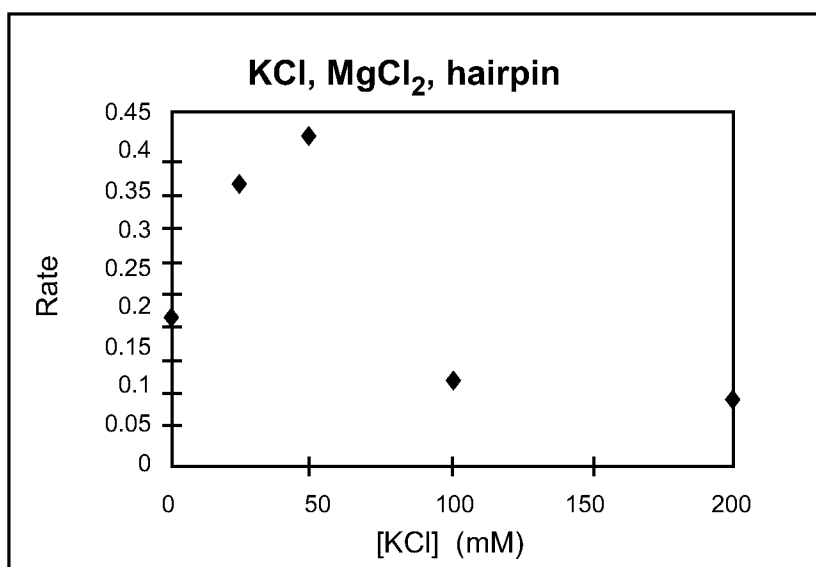


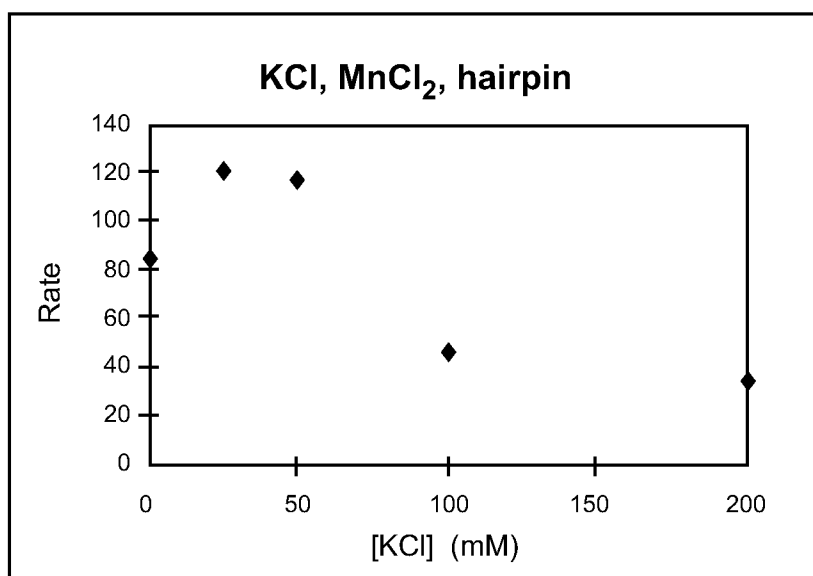
**FIG. 105I**

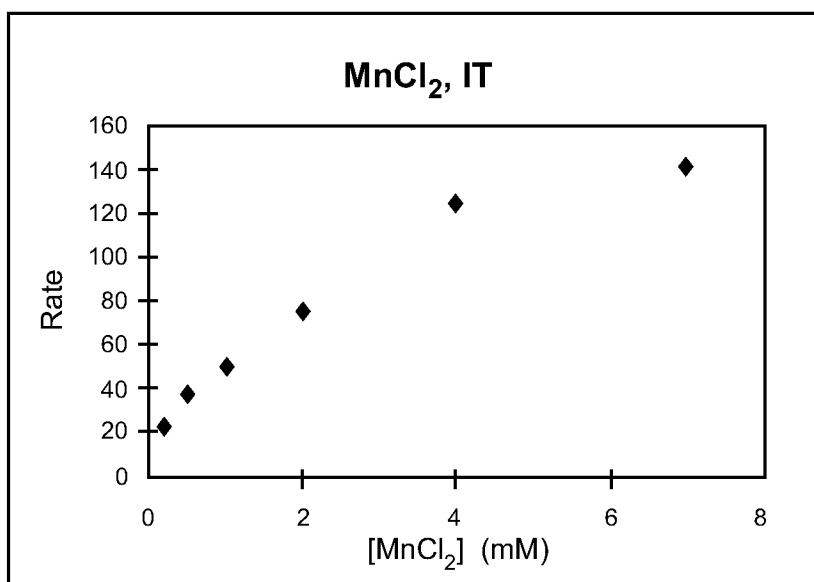
**FIG. 105J**

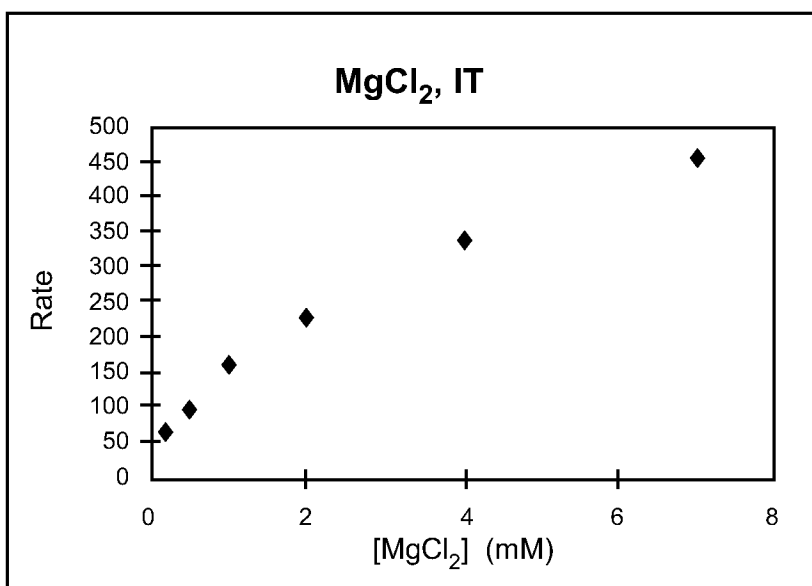
**FIG. 106A**

**FIG. 106B**

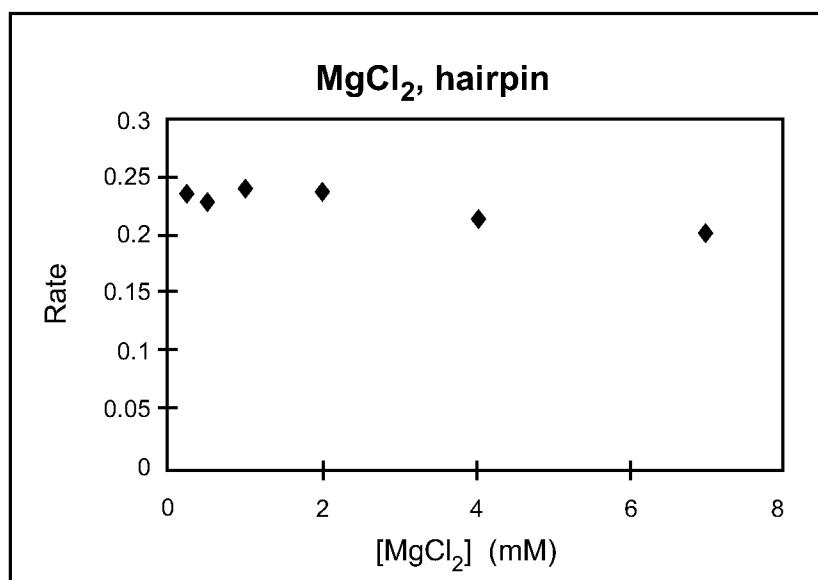
**FIG. 106C**

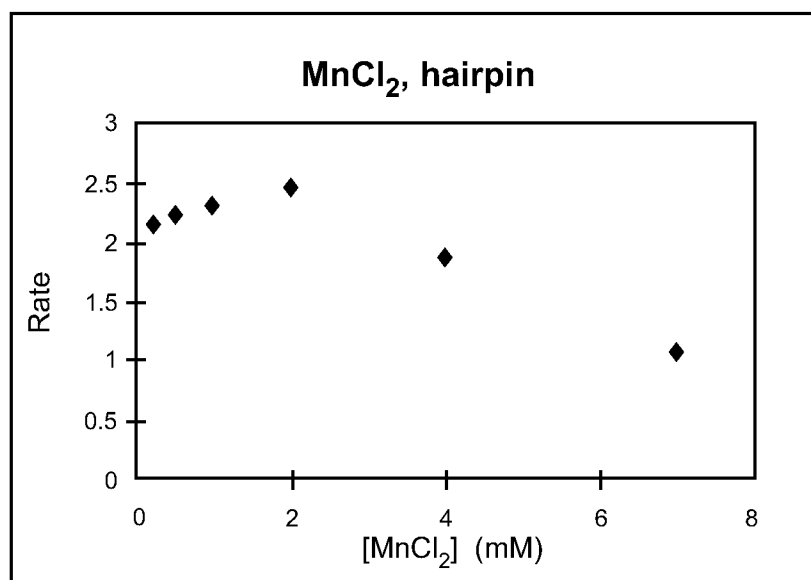
**FIG. 106D**

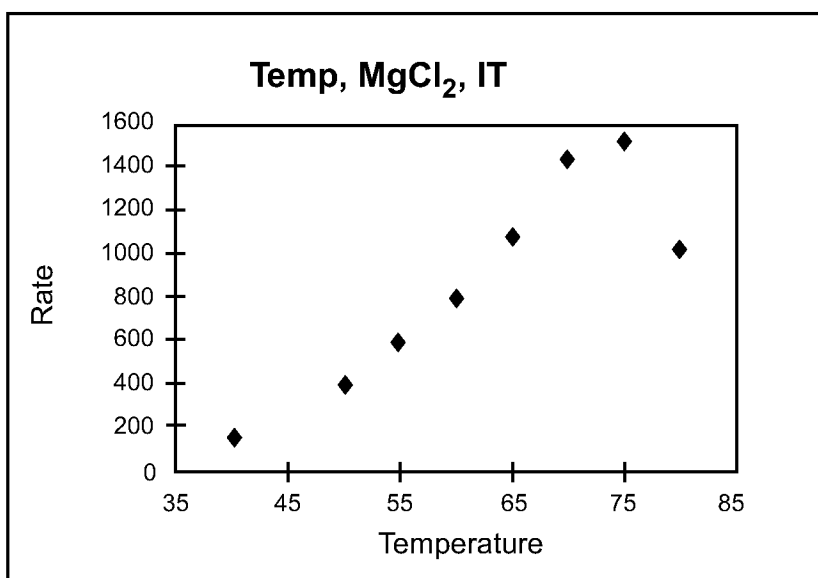
**FIG. 106E**

**FIG. 106F**



**FIG. 106G**

**FIG. 106H**

**FIG. 106I**

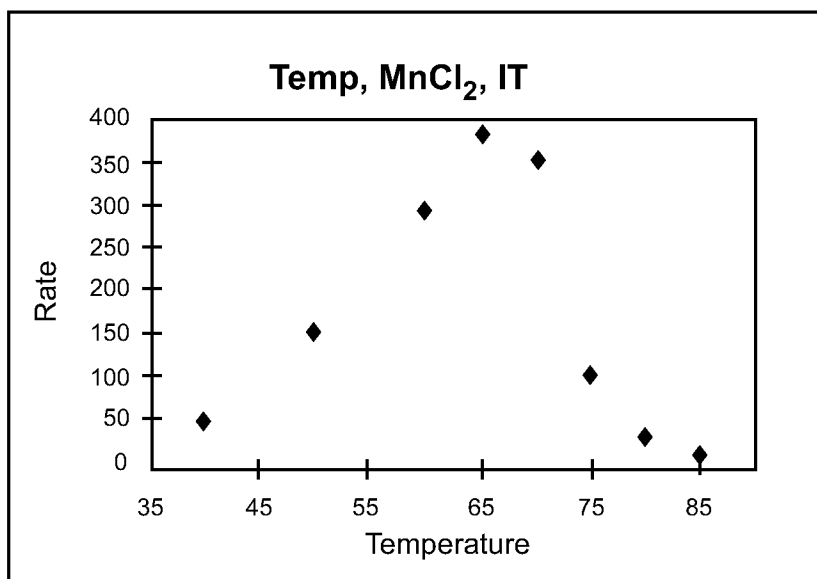
**FIG. 106J**

FIGURE 107

